

**Port, Toby**

---

**From:** Swope, Sheridan  
**Sent:** Monday, July 18, 2005 11:49 AM  
**To:** Port, Toby  
**Subject:** FW: 10/674,636

I do not have the results from this search request.  
Was it completed?  
Would you send me the results?

-----Original Message-----

**From:** STIC-Biotech/ChemLib  
**Sent:** Monday, July 18, 2005 11:39 AM  
**To:** Swope, Sheridan  
**Subject:** RE: 10/674,636

Call 22523 Toby Port.

-----Original Message-----

**From:** Swope, Sheridan  
**Sent:** Monday, July 18, 2005 11:23 AM  
**To:** STIC-Biotech/ChemLib  
**Subject:** FW: 10/674,636

Who has this search request?

-----Original Message-----

**From:** Swope, Sheridan  
**Sent:** Wednesday, June 15, 2005 3:59 PM  
**To:** STIC-Biotech/ChemLib  
**Subject:** 10/674,636

For 10/674,636, pls search and interference search:

SID 2 regular full-length against the AA databases

SID 2 oligo search ( $\geq 50$  AAs) against the AA databases

THANKS!!

Sheridan Swope, Ph.D.  
Patent Examiner, AU 1652  
Recombinant Enzymes  
571-272-0943 (voice)  
E02B71 Remsen Bld (Office)  
E02C70 Remsen Bld (Mailbox)

T. Port

***This Page Blank (uspto)***

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 20:19:15 ; Search time 167 Seconds  
(without alignments)  
1345.556 Million cell updates/sec

Title: US-10-674-636-2

Perfect score: 3079  
Sequence: 1 MPQGLTSSASQWCFFLLIQP.....PLSSLTFLSLIQPPFFFCAP 581

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_1dDec04:\*

1: geneeqp1980s:\*\n2: geneeqp1990s:\*\n3: geneeqp2000s:\*\n4: geneeqp2001s:\*\n5: geneeqp2002s:\*\n6: geneeqp2003as:\*\n7: geneeqp2003bs:\*\n8: geneeqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	* Query Match	Length	ID	Description
1	3079	100.0	581	5	ABR79537 Human car
2	3079	100.0	581	8	ADQ89094 Human uro
3	2915	94.7	575	5	ABP61004 Novel hum
4	2900	94.2	642	5	AAE25025 Human dlu
5	2900	94.2	642	8	ABM84114 Human dia
6	2607.5	84.7	581	5	ABP61005 Novel hum
7	2606	84.6	525	6	ADA54807 Human pro
8	2597.5	84.4	581	6	ABU54639 Human NOV
9	2588.5	84.1	618	5	ADR19663 Human dtr
10	2454	79.7	469	7	ADB64065 Human pro
11	1985	64.5	542	8	ADR50145 Cat cauxi
12	1985	64.5	542	8	ADR50147 Cat cauxi
13	1780	57.8	356	5	ABP61006 Novel hum
14	1262.5	41.0	561	3	AAE20911 Rat carbo
15	1230	39.9	549	3	AAE58981 Breast an
16	1230	39.9	550	8	ADG98219 Human int
17	1230	39.9	559	4	AAE31700 Protein e
18	1230	39.9	559	4	ABU53223 Human met
19	1230	39.9	559	6	ABR82851 CES2 rela
20	1230	39.9	559	6	AAE33960 Human pro
21	1230	39.9	559	7	ADD46521 Human car
22	1231	39.7	306	5	AAE20909 Human car
23	1213.5	35.4	561	7	ADD46519 Rat Prote
24	1191	38.7	607	4	ABU53222 Human met
25	1186.5	38.5	554	8	ADI79890 Mouse liv

26	1181	38.4	583	4	ABG10273	ABG10273	Novel hum
27	1179.5	38.3	571	3	AAV71107	AAV71107	Human Hyd
28	1179.5	38.3	571	4	AAU12442	AAU12442	Human PRO
29	1179.5	38.3	571	4	AAE04101	AAE04101	Human gen
30	1179.5	38.3	571	5	AAU83696	AAU83696	Human PRO
31	1179.5	38.3	571	5	ABR84949	ABR84949	Human PRO
32	1179.5	38.3	571	5	ABG64341	ABG64341	Human alb
33	1179.5	38.3	571	6	ABO17886	ABO17886	Novel hum
34	1179.5	38.3	571	6	ABU69108	ABU69108	Human PRO
35	1179.5	38.3	571	6	ABU80843	ABU80843	Human PRO
36	1179.5	38.3	571	6	ABO33809	ABO33809	Novel hum
37	1179.5	38.3	571	6	ABU81140	ABU81140	Human PRO
38	1179.5	38.3	571	6	ABO19424	ABO19424	Human sec
39	1179.5	38.3	571	6	ABU68840	ABU68840	Human PRO
40	1179.5	38.3	571	6	ABU59921	ABU59921	Novel sec
41	1179.5	38.3	571	6	ABU69085	ABU69085	Human PRO
42	1179.5	38.3	571	6	ABO25111	ABO25111	Human sec
43	1179.5	38.3	571	6	ABU82152	ABU82152	Novel hum
44	1179.5	38.3	571	6	ABU67116	ABU67116	Human sec
45	1179.5	38.3	571	6	ABU81549	ABU81549	Human sec

#### ALIGNMENTS

RESULT 1	ABR79537	
ID	ABR79537 standard; protein; 581 AA.	
XX		
AC	ABR79537;	
DT	23-SEP-2002 (first entry)	
XX		
DE	Human carboxylesterase family member 53010.	
XX		
KM	Carboxylesterase; enzyme; human; analgesic; nootropic; antiinflammatory;	
XX	diagnosis; therapy.	
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	Peptide	1..26
FT	Protein	/label= Signal_peptide
FT	Domain	27..581
FT		/label= Mature_protein
FT	Region	44..545
FT	Active-site	/note= "carboxylesterase domain"
FT		125..135
FT		/note= "predicted carboxylesterase type-B signature"
FT		219..234
FT		/note= "predicted carboxylesterase type-B serine active site"
XX		
PD	27-JUN-2002.	
XX		
PF	18-DEC-2001; 2001WO-US049075.	
XX		
PR	18-DEC-2000; 2000US-0256369P.	
XX		
PR	28-MAR-2001; 2001US-0279508P.	
XX		
PA	(MILL-) MILLENNIUM PHARM INC.	
XX		
PI	Curtis RAJ, Silos-Santiago I;	
XX		
DR	WPI; 2002-547936/58.	
XX		
DR	N-PSDB; ABR84302.	
XX		
PT	53010 nucleic acids, useful for diagnosing and treating e.g. vascular	
XX	diseases, autoimmune diseases, or neurodegenerative diseases, as	
XX	surrogate markers, in tissue typing and chromosome mapping.	

PS Claim 5; Page 110-111; 122pp; English.

XX The present sequence is the protein sequence of human 53010, a novel  
CC protein containing the structural characteristics of a carboxylesterase  
CC family member. The invention provides 53010 nucleic acids, antisense  
CC molecules, expression vectors, host cells, transgenic animals, 53010  
CC proteins, fusion proteins, antigenic peptides, anti-53010 antibodies and  
CC methods for detecting the presence of 53010 polypeptides or nucleic  
CC acids, of identifying a compound that binds to the 53010 polypeptide and  
CC of modulating the activity of the polypeptide. The 53010 polypeptide, and  
CC nucleic acids can act as novel diagnostic and therapeutic agents for  
CC controlling disorders involving aberrant or deficient hydrolysis of  
CC carboxylic esters. As 53010 mRNA is highly expressed in the central and  
CC peripheral nervous system, and its expression is regulated in some rodent  
CC pain models, 53010 molecules can also act as novel diagnostic targets and  
CC therapeutic agents for controlling neurological disorders, such as pain-  
CC related disorders. A claimed method of treating or preventing a disorder  
CC (especially a pain-related disorder) characterized by aberrant activity  
CC of a 53010-expressing cell involves administering a compound that  
CC modulates 53010 activity or expression  
XX

SQ Sequence 581 AA;

Query Match 100.0%; Score 3079; DB 5; Length 581;  
Best Local Similarity 100.0%; Pred. No. 1e-278;

Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPOGLTSSASQWCFLLIOLPLGHRWGKTPSAGEPQNTRLGWTQKQVTVLGSPPV 60  
DB 1 MPOGLTSSASQWCFLLIOLPLGHRWGKTPSAGEPQNTRLGWTQKQVTVLGSPPV 60  
QY 61 NVFLGVFPFAAPPLGSRFTNPPQASPMWDLREATSYPNLCLQNSWMLLDQHMVKVYRK 120  
DB 61 NVFLGVFPFAAPPLGSRFTNPPQASPMWDLREATSYPNLCLQNSWMLLDQHMVKVYRK 120  
QY 121 FGVEDCLYNTIYAPAHADTGSRLPVLPFGAGAKTGSASIFGSAALAAVEDLVVVVVO 180  
DB 121 FGVEDCLYNTIYAPAHADTGSRLPVLPFGAGAKTGSASIFGSAALAAVEDLVVVVVO 180  
QY 122 FGVEDCLYNTIYAPAHADTGSRLPVLPFGAGAKTGSASIFGSAALAAVEDLVVVVVO 180  
DB 122 FGVEDCLYNTIYAPAHADTGSRLPVLPFGAGAKTGSASIFGSAALAAVEDLVVVVVO 180  
QY 181 YRLGIFGFFTTWDQAHAPGNMAFKQVAALSWQKIEFPGDPSVYIRGESAGATSVS 240  
DB 181 YRLGIFGFFTTWDQAHAPGNMAFKQVAALSWQKIEFPGDPSVYIRGESAGATSVS 240  
QY 241 LILSPMAGLPHKAIMESGVAIIPYLEAHNDYKESDQVVAHFCGNNAADSEALRLCLRT 300  
DB 241 LILSPMAGLPHKAIMESGVAIIPYLEAHNDYKESDQVVAHFCGNNAADSEALRLCLRT 300  
QY 301 KPSKELTLTSGKTSFTRVVDGAFEPNEPDLISOKAFKAIPIIIGVNNHCGFLPMKE 360  
DB 301 KPSKELTLTSGKTSFTRVVDGAFEPNEPDLISOKAFKAIPIIIGVNNHCGFLPMKE 360  
QY 361 APELISGNSKSLAHLONILHLPQYLHVANEYFHDKSLTEIRDSLIDLGLGVFPV 420  
DB 361 APELISGNSKSLAHLONILHLPQYLHVANEYFHDKSLTEIRDSLIDLGLGVFPV 420  
QY 421 PALITARYHDAGAPVYFEFRHRPOCFEDTKPAFKADHAEVFPVGGALDKEDYMF 480  
DB 421 PALITARYHDAGAPVYFEFRHRPOCFEDTKPAFKADHAEVFPVGGALDKEDYMF 480  
QY 481 EGATEERKLSRQMKCYATFARTGNPNNDLSLMPAYMLTEQYLQDLNLSLQRLKEP 540  
DB 481 EGATEERKLSRQMKCYATFARTGNPNNDLSLMPAYMLTEQYLQDLNLSLQRLKEP 540  
QY 541 RVDFTWSTIPLILSADMLSPSLTFLSLQPEFFCAP 581  
DB 541 RVDFTWSTIPLILSADMLSPSLTFLSLQPEFFCAP 581

RESULT 2  
ADQ89094  
ID ADQ89094 standard; protein; 581 AA.  
XX  
AC ADQ89094;

XX 21-OCT-2004 (first entry)

XX Human urological disorder related protein 53010 SEQ.46.

XX urological disorder; uropathic; cytoskeletal; urinary incontinence;  
XX benign prostatic hyperplasia; human.

XX Homo sapiens.

XX WO2004065576-A2.

XX 05-AUG-2004.

XX 14-JAN-2004; 2004MO-US000750.

XX 15-JAN-2003; 2003US-0440318P.

XX 04-FEB-2003; 2003US-0444783P.

XX 27-MAR-2003; 2003US-0457901P.

XX 08-MAY-2003; 2003US-0468775P.

XX 19-MAY-2003; 2003US-0471614P.

XX 16-JUN-2003; 2003US-0478742P.

XX 18-JUL-2003; 2003US-0488529P.

XX 30-JUL-2003; 2003US-0491155P.

XX 02-SEP-2003; 2003US-0495594P.

XX 26-SEP-2003; 2003US-0506332P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Karichevi V, Siles-Santiago I, Eliasof SD;

XX WPI; 2004-562167/54.

XX N-PSDB; ADQ89093.

XX Use of polypeptides related to urological disorders, e.g. 44390, 54181,

XX 211 or for identifying a compound capable of treating a urological

XX disorder or identifying and treating a subject having a urological

XX disorder.

XX Claim 1; SEQ ID NO 46; 542pp; English.

XX The present invention describes the use of polypeptides related to

XX urological disorders for identifying a compound capable of treating a

XX urological disorder, identifying a subject having a urological disorder,

XX or treating a subject having a urological disorder. Also described: (1) a

XX method for identifying a compound capable of treating a urological

XX disorder; (2) a method for identifying a subject having a urological

XX disorder; and (3) a method for treating a subject having a urological

XX disorder. The compound has uropathic and cytoskeletal activities. The

XX polypeptides related to urological disorders are useful for identifying a

XX compound capable of treating a urological disorder, identifying a subject

XX having a urological disorder, or treating a subject having a urological

XX disorder. Disorders include urinary incontinence and benign prostatic

XX hyperplasia. The present sequence represents a human urological disorder

XX related protein, which is used in the exemplification of the present

SQ Sequence 581 AA;

Query Match 100.0%; Score 3079; DB 8; Length 581;  
Best Local Similarity 100.0%; Pred. No. 1e-278;

Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPOGLTSSASQWCFLLIOLPLGHRWGKTPSAGEPQNTRLGWTQKQVTVLGSPPV 60  
DB 1 MPOGLTSSASQWCFLLIOLPLGHRWGKTPSAGEPQNTRLGWTQKQVTVLGSPPV 60  
QY 61 NVFLGVFPFAAPPLGSRFTNPPQASPMWDLREATSYPNLCLQNSWMLLDQHMVKVYRK 120  
DB 61 NVFLGVFPFAAPPLGSRFTNPPQASPMWDLREATSYPNLCLQNSWMLLDQHMVKVYRK 120  
QY 121 FGVEDCLYNTIYAPAHADTGSRLPVLPFGAGAKTGSASIFGSAALAAVEDLVVVVVO 180  
DB 121 FGVEDCLYNTIYAPAHADTGSRLPVLPFGAGAKTGSASIFGSAALAAVEDLVVVVVO 180



```

Db      121 FGVEBDCLYNIYAPAHADTGSKLFLVWFGGAFKTSASIFDGSALAAVEDLVVVVV 180
Oy      181 YRLGIFGFTTWDQHPAGNMAFKDOVALSWQKNIIEFGGDPSSVTITFGSAGASIVSS 240
Db      181 YRLGIFGFTTWDQHPAGNMAFKDOVALSWQKNIIEFGGDPSSVTITFGSAGASIVSS 240
Oy      241 LIISPMAGLFFHKAIMESGVAIIPYLEAHDYKESDLOVVAHFCGNNASDEBALIRCLRT 300
Db      241 LIISPMAGLFFHKAIMESGVAIIPYLEAHDYKESDLOVVAHFCGNNASDEBALIRCLRT 300
Oy      301 KPSKELLTSLQKTSFTRVVDGAFPPNEPDLISQAKAKAPSIIGVNNHCGFLIPMKE 360
Db      301 KPSKELLTSLQKTSFTRVVDGAFPPNEPDLISQAKAKAPSIIGVNNHCGFLIPMKE 360
Oy      361 APELISGNSKSLAHLIONIHLIPPOYLVAANEYFHDKSLTEIRDSLDLQGVFFV 420
Db      361 APELISGNSKSLAHLIONIHLIPPOYLVAANEYFHDKSLTEIRDSLDLQGVFFV 420
Oy      421 PALITARYHARDAGAFVYFEFRHRPQCFEDTKPAFVKADHDEVFVFGAFLKGDIVMF 480
Db      421 PALITARYHARDAGAFVYFEFRHRPQCFEDTKPAFVKADHDEVFVFGAFLKGDIVMF 480
Oy      481 EGATBEERKLSRKKMKYATPARGNPNNGNDLSLMPANVLEOYLQDLNLSLQRLKEP 540
Db      481 EGATBEERKLSRKKMKYATPARGNPNNGNDLSLMPANVLEOYLQDLNLSLQRLKEP 540
Oy      541 RVDFWTSITPILASDMHSPLSLTLTSLLOPFFPCAP 581
Db      541 RVDFWTSITPILASDMHSPLSLTLTSLLOPFFPCAP 581

```

## RESULT 3

ABP61004 standard; protein, 575 AA.

ABP61004;  
10-SEP-2002 (first entry)

Novel human protein. SEQ ID 91.

Human; cytostatic; vulnary; antiarteriosclerotic; antiparkinsonian;  
neurotropic; neuroprotective; immunosuppressive; haemostatic;  
antiinflammatory; cardiatic; antitumor; virucide; antihydrolyd;  
cerebroprotective; anorectic; metabolic; vaccinate; cancer; infection;  
wound healing disorders; atherosclerosis; Parkinson's disease;  
Alzheimer's disease; autoimmune disorder; haematopoietic disorder;  
inflammation; neoplastic disease; nervous system disorder;  
cardiovascular disorder; pancreatitis; respiratory disorder;  
hyperproliferation; systemic autoimmune disease; hyper-immunity;  
developmental abnormality; gastrointestinal ulceration; neuropathy;  
haematological disease; metabolic disease; sperm dysfunction;  
thyroid disorder; hypothyroidism; brain damage; colitis;  
cone photo- transduction deficiency; neurological disease; stroke;  
angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;  
trachea; thymus; lymph node; muscular system; obesity; anorexia;  
growth abnormality; precocious puberty.

Homo sapiens.  
WO200250105-A1.  
27-JUN-2002.  
17-DEC-2001; 2001WO-US049232.  
19-DEC-2000; 2000US-0256710P.  
20-DEC-2000; 2000US-0257048P.  
09-JAN-2001; 2001US-0260483P.  
30-JAN-2001; 2001US-0264922P.  
06-FEB-2001; 2001US-0266797P.  
19-MAR-2001; 2001US-0276988P.  
04-APR-2001; 2001US-0281535P.

08-MAY-2001; 2001US-0289622P.  
(SMIK ) SMITHKLINE BEECHAM CORP.  
(SMIK ) SMITHKLINE BEECHAM PLC.  
(GLAX ) GLAXO GROUP LTD.  
Agarwal P, Birkeland M, Cogswell JP, Kabnick KF, Lai Y;  
Mattenen SA, Rizvi SK, Smith RF, Strum JC, Xie Q;  
WPI; 2002-508784/54.  
N-PSDB; ABQ86169.  
Secreted proteins and polynucleotides useful as vaccines for preventing  
or treating various diseases e.g. cancer, wounds, atherosclerosis,  
Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.  
Claim 1(a); Page 312-313; 335pp; English.

The invention relates to an isolated polypeptide with signal sequences  
which allow it to be secreted extracellularly or membrane associated. The  
activity of polypeptides of the invention may be described as,  
cytostatic, vulnary, antiarteriosclerotic, antiparkinsonian, neurotropic,  
neuroprotective, immunosuppressive, haemostatic, antiinflammatory,  
cardiant, antitumor, virucide, antihydrolyd, cerebroprotective, anorectic,  
and metabolic. Polypeptides and polynucleotides of the invention are  
useful in the treatment, or as a vaccine in the prevention of, cancer,  
wound healing disorders, infection, atherosclerosis, Parkinson's disease  
and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,  
inflammation, neoplastic diseases, nervous system related disorders and  
cardiovascular disorders, pancreatitis, respiratory disorder,  
hyperproliferation, systemic autoimmune disease, hyper-immunity,  
developmental abnormality, gastrointestinal ulceration, neuropathy,  
haematological diseases, metabolic diseases, sperm dysfunction, thyroid  
disorders e.g. hypothyroidism, brain damage, colitis, cone photo-  
transduction deficiency, neurological diseases, stroke, angiogenesis,  
ovulation disorders, diseases in the spinal cord, thyroid gland, heart,  
trachea, thymus, lymph node and muscular system, obesity, anorexia,  
growth abnormalities, and alleviation of precocious puberty. The  
sequences given in records ABP60965-ABP61019 represent novel human  
proteins of the invention

Sequence 575 AA;

Query Match 94.7%; Score 2915; DB 5; Length 575;  
Best Local Similarity 97.0%; Pred. No. 2.3e-263;  
Matches 553; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

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Oy      12 WCPFLIQPLIGHROWGKTGSAGGPOBNTRLGIIQKQVTVLGGSPVNVNPLGVPPAP 71
Db      14 WAIWVLAAP-----TKGPSAEGPQNRTRLGIQKQVTVLGGSPVNVNPLGVPPAP 65
Oy      72 PLGSLRFPNPPASPMNLTREATSYPNLCLONSMWLLDDQMLVHYPKPVSEDCLYLN 131
Db      66 PLGSLRFPNPPASPMNLTREATSYPNLCLONSMWLLDDQMLVHYPKPVSEDCLYLN 125
Oy      132 IYAPAHADTGSKLFLVWFGGAFKTSASIFDGSALAAVEDLVVVVQYRLGIFGFTT 191
Db      126 IYAPAHADTGSKLFLVWFGGAFKTSASIFDGSALAAVEDLVVVVQYRLGIFGFTT 185
Oy      192 WDOHAPGNMAFKDOVAALSWQKNIIEFGGDPSSVTITFGSAGASIVSSLIISPMAGLF 251
Db      186 WDOHAPGNMAFKDOVAALSWQKNIIEFGGDPSSVTITFGSAGASIVSSLIISPMAGLF 245
Oy      252 HKATMESGVAIIPYLEAHDYKESDLOVVAHFCGNNASDEBALIRCLRTKSKELLTSLQ 311
Db      246 HKATMESGVAIIPYLEAHDYKESDLOVVAHFCGNNASDEBALIRCLRTKSKELLTSLQ 305
Oy      312 KTKSFTRVVDGAFPPNEPDLISQAKAKAPSIIGVNNHCGFLIPMKEAPEILSGSNKS 371
Db      306 KTKSFTRVVDGAFPPNEPDLISQAKAKAPSIIGVNNHCGFLIPMKEAPEILSGSNKS 365
Oy      372 LALHLIONIHLIPPOYLVAANEYFHDKSLTEIRDSLDLQGVFFVVPALITARYHARD 431

```

Db 366 LALHLIIONIIHPQYILVANEYFHDKSLTEIRDSLLDLGDFVFPVPLITARYRD 425  
 Qy 432 AGAPVTFYFERRHPOCFEDTKPAFVADHAEVRFVFGAFLKGDIVFEGATEBEKLLS 491  
 Db 426 AGAPVTFYFERRHPOCFEDTKPAFVADHAEVRFVFGAFLKGDIVFEGATEBEKLLS 485  
 Qy 492 RKMKKWATFARTGNNGNDLSLMPAYNLTEQYLOLDINMSLQRLKEPRVDFWTSTIPL 551  
 Db 486 RKMKKWATFARTGNNGNDLSLMPAYNLTEQYLOLDINMSLQRLKEPRVDFWTSTIPL 545  
 Qy 552 ILSASDMLHSPSLSTFLSLQPFPPFCAP 581  
 Db 546 ILSASDMLHSPSLSTFLSLQPFPPFCAP 575

RESULT 4  
 AAE25025  
 ID AAE25025 standard; protein, 642 AA.  
 AC AAE25025;  
 XX  
 DT 30-OCT-2002 (first entry)  
 XX  
 DE Human drug metabolizing enzyme (DME-10).  
 XX  
 KW Human; drug metabolizing enzyme; autoimmune; inflammatory disorder;  
 KW acquired immunodeficiency syndrome; AIDS; atherosclerosis; psoriasis;  
 KW proliferative disorder; arteriosclerosis; cirrhosis; hepatitis; cancer;  
 KW dementia; Parkinson's disease; development disorder; anaemia; adenoma;  
 KW drug screening; endocrine disorder; conjunctivitis; glaucoma; cataract;  
 KW renal tubular acidosis; eye disorder; epilepsy; thrombosis; peptic ulcer;  
 KW anorexia; metabolic disorder; cystic fibrosis; diabetes; liver disorder;  
 KW goitre; gastrointestinal disorder; gene therapy; viroicide; anticoagulant;  
 KW anticonvulsant; nootropic; enzyme; DME-10.  
 XX  
 OS Homo sapiens.

XX  
 XX Key Location/Qualifiers  
 FH Peptide 1..50  
 FT /label=Signal\_peptide  
 FT Domain 32..56  
 FT /note="Transmembrane domain"  
 FT Protein 51..642  
 FT /note="Mature human DME-10"  
 FT Domain 113..135  
 FT /note="Transmembrane domain"  
 FT Domain 204..220  
 FT /note="Transmembrane domain"  
 FT Domain 234..250  
 FT /note="Transmembrane domain"  
 FT Domain 287..314  
 FT /note="Transmembrane domain"  
 FT Domain 463..491  
 FT /note="Transmembrane domain"  
 PN WO200246426-A2.  
 XX  
 PD 13-JUN-2002.  
 XX  
 PF 04-DEC-2001; 2001WO-US047429.  
 XX  
 PR 08-DEC-2000; 2000US-0254308P.  
 PR 15-DEC-2000; 2000US-0256189P.  
 PR 21-DEC-2000; 2000US-0257713P.  
 PR 19-JAN-2001; 2001US-0262706P.  
 PR 02-FEB-2001; 2001US-0266020P.  
 XX  
 XX (INCY-) INCYTE GENOMICS INC.

PI Sanjanwala MM, Yao MG, Au-Young J, Baughn MR, Arvizu C, Ring HZ,  
 PI Lee EA, Ding L, Hafalia ABA, Tang YT, Yue H, Tribouley CM, Lu DM,  
 PI Lal PG, Warren BA, Yang J, Walla NK, Nguyen DB, Gandhi AR, Lu Y;

PI Ieon CH;  
 XX  
 DR MPI: 2002-519668/55.  
 DR N-PSDB: AAD40574.  
 XX  
 PT Novel human drug metabolizing polypeptide, useful in diagnosis,  
 PT prevention or treatment of autoimmune/inflammatory, cell proliferative,  
 PT neurological, developmental, endocrine, metabolic and gastrointestinal  
 disorders.  
 XX  
 PS Claim 65; Page 155-156; 169pp; English.

XX  
 CC The invention relates to an isolated human drug metabolizing enzyme (DME)  
 CC and its nucleotide. DME is useful for diagnosing, treating or preventing  
 CC disorders associated with aberrant expression of DME, where the disorders  
 CC are selected from autoimmune/inflammatory disorder such as acquired  
 CC immunodeficiency syndrome (AIDS), asthma, atherosclerosis, psoriasis,  
 CC cirrhosis, hepatitis, and cancer; a neurological disorder such as  
 CC Alzheimer's disease, Huntington's disease, dementia, Parkinson's disease;  
 CC a developmental disorder such as renal tubular acidosis, epilepsy,  
 CC anaemia; an endocrine disorder such as adenoma, thrombosis and infections  
 CC ; an eye disorder such as conjunctivitis, diabetes and goitre; a gastrointestinal  
 CC disorder such as cystic fibrosis, diabetes and goitre; a gastrointestinal  
 CC disorder such as anorexia, peptic ulcer, and liver disorders. DME is  
 CC useful in a number of drug screening techniques and to analyze the  
 CC proteome of a tissue or cell type. The invention is useful for creating  
 CC knock-in humanised animals or transgenic animals to model human diseases,  
 CC in somatic or germline gene therapy, to generate a transcript image of a  
 CC tissue or cell type, for detecting differences in the chromosomal  
 CC location due to translocation, inversion, etc. among normal, carrier or  
 CC affected individuals, and as hybridisation probes for mapping naturally  
 CC occurring genomic sequences. The present sequence is human DME-10  
 CC  
 XX

Sequence 642 AA:

Query Match 94.2%; Score 2900; DB 5; Length 642;  
 Best Local Similarity 99.5%; Pred. No. 7e-262;  
 Matches 548; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 31 GPSAEGPQRTKRGWIGQVTVLGSPPVNVFLGVPPAAPLGLRTFNPQPSPMNLT 90  
 Db 92 GPSAEGPQRTKRGWIGQVTVLGSPPVNVFLGVPPAAPLGLRTFNPQPSPMNLT 151  
 Qy 91 REATSYPNLCLQNSEMLLDQHLKVHYPKRGVSDCLYLYTYPAHADTSGKLPVLVWF 150  
 Db 152 REATSYPNLCLQNSEMLLDQHLKVHYPKRGVSDCLYLYTYPAHADTSGKLPVLVWF 211  
 Qy 151 PGGAFTGASIFDGSALAAVEDVLVVVQYRLGIFGFTTWDQAHAGNNAFDOVAAIS 210  
 Db 212 PGGAFTGASIFDGSALAAVEDVLVVVQYRLGIFGFTTWDQAHAGNNAFDOVAAIS 271  
 Qy 211 WQKNIIEFGDPPSSVTIFGESAGNISVSSLILSPMKGLFHAQINESGVAILPYLEAHD 270  
 Db 272 WQKNIIEFGDPPSSVTIFGESAGNISVSSLILSPMKGLFHAQINESGVAILPYLEAHD 331  
 Qy 271 YKESDLOVNAHFGGNNAADSEALLRCLRTKPSKELLTLISQKTSFTRVVDGAFPNPBL 330  
 Db 332 YKESDLOVNAHFGGNNAADSEALLRCLRTKPSKELLTLISQKTSFTRVVDGAFPNPBL 391  
 Qy 331 DLSQKAFKALPSIIGVNNHCEGFLPMKEAPRILSGSKSLALHLIIONIIHPQYILH 390  
 Db 332 DLSQKAFKALPSIIGVNNHCEGFLPMKEAPRILSGSKSLALHLIIONIIHPQYILH 451  
 Qy 391 VANEYFHDKSLTEIRDSLLDLGDFVFPVPLITARYYRDGAPVYFEPFRHPOCFED 511  
 Db 452 VANEYFHDKSLTEIRDSLLDLGDFVFPVPLITARYYRDGAPVYFEPFRHPOCFED 511  
 Qy 451 TKPAFVADHAEVRFVFGAFLKGDIVFEGATEBEKLLSRKMKKWATFARTGNNGN 510  
 Db 512 TKPAFVADHAEVRFVFGAFLKGDIVFEGATEBEKLLSRKMKKWATFARTGNNGN 571  
 Qy 511 DLSLMPAYNLTEQYLOLDINMSLQRLKEPRVDFWTSTIPLILSASDMLHSPSLSTFLS 570

DB 572 DLFLMPAYNLTQYLQDLNMSLQRLKEPRVFWTSTIPILISASDMLSPSLTFLS 631  
 QY 571 LLOPFFFCAP 581  
 DB 632 LLOPFFFCAP 642

RESULT 5  
 ABM64114  
 ID ABM64114 standard; protein: 642 AA.

AC ABM64114;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pprotein SEQ ID NO:4363.

XX gene therapy; human diagnostic and therapeutic polynucleotide; dthp.

OS Homo sapiens.

XX WO2004023973-A2.

PD 25-MAR-2004.

PF 12-SEP-2003; 2003WO-US028227.

PR 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

PA (INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

PI Hartsbome TA, Suchnorski MT, Altus CM, Pitts SJ, Elder LV;

PI Mooney EM, Deleagne AM, Panesar IS, Banville SC, Reddy TP;

PI Stevens KM, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstl EH;

PI Peralta CH, Anderson SB, Ricou P, Shen EJ, Wu MC, Stuve LL;

PI Lagace RE, Spito PA, Stewart EA, Wingrove J, Vilt UA, Kirton ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

PI Patry S, Shi X, Suarez CJ;

XX Claim 27; Page: 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides

XX selected from one of the 2722 sequences defined in the specification. A

XX polynucleotide of the invention may have a use in gene therapy. The human

XX diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be

XX used to diagnose a particular condition, disease or disorder associated

XX with human molecules, e.g. cell proliferative disorders, endocrine

XX autoimmune/inflammatory disorder, developmental disorder, endocrine

XX disorder, neurological disorders, gastrointestinal disorders, or

XX infections caused by virus, bacteria, fungi or parasite. The dthp

XX molecules may also be used in genetic mapping, in identifying individuals

XX from minute biological samples, in detecting single nucleotide

XX polymorphisms, as molecular weight markers, and for somatic or germline

XX gene therapy. The present sequence represents a dthp protein of the

XX invention. Note: The sequence data for this patent is not represented in

XX the printed specification, but was obtained in electronic format directly

XX from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

XX Sequence 642 AA;

XX Query Match 94.2%; Score 2900; DB 8; Length 642;

XX Best Local Similarity 99.6%; Pred. No. 7e-262;

Matches 549; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 31 GPSAEGPQNTRLGQVTLGSPVNVFLGVFAAPPGSLFTNPQASPMNDL 90

DB 92 GPSAEGPQNTRLGQVTLGSPVNVFLGVFAAPPGSLFTNPQASPMNDL 151

QY 91 REATSYNCLQNSEWLLDQNMKHYPRGVSBDCLYNTYPAADGSKLPVYWF 150

DB 152 REATSYNCLQNSEWLLDQNMKHYPRGVSBDCLYNTYPAADGSKLPVYWF 211

QY 151 PGAFKTSASIFPGSALAAVEDLVVYVQYRGIFGFPTTMDQAHGNAFKDQVALS 210

DB 212 PGAFKTSASIFPGSALAAVEDLVVYVQYRGIFGFPTTMDQAHGNAFKDQVALS 271

QY 211 WQKNIEFFGDPSSVTIIPESAGALSIVSSILSPMAKGFEHKAIMSGVAIIPYLEAD 270

DB 272 WQKNIEFFGDPSSVTIIPESAGALSIVSSILSPMAKGFEHKAIMSGVAIIPYLEAD 331

QY 271 YEKSEDLQVVAHFCGNASDSEALLRCLRTKPSKELLTSQTKSFTRVVDGAFPMNEPL 330

DB 332 YEKSEDLQVVAHFCGNASDSEALLRCLRTKPSKELLTSQTKSFTRVVDGAFPMNEPL 391

QY 331 DLISOKAFKALPSIIGVNNHCGFLPMKEAPEILSGSNKSLAHLIQLIHLIPPOYLHL 390

DB 392 DLISOKAFKALPSIIGVNNHCGFLPMKEAPEILSGSNKSLAHLIQLIHLIPPOYLHL 451

QY 391 VANEYFHDKSLTEIRPSLLDLGDVFEVVPALITARYHDAGAPVYFEYERHPOCED 450

DB 452 VANEYFHDKSLTEIRPSLLDLGDVFEVVPALITARYHDAGAPVYFEYERHPOCED 511

QY 451 TKPAFVADHAEVRFVFGAFLKGDIVMEGATEEKKLSRKMKYATFARTGNPNGN 510

DB 512 TKPAFVADHAEVRFVFGAFLKGDIVMEGATEEKKLSRKMKYATFARTGNPNGN 571

QY 511 DLSTMPAYNLTQYLQDLNMSLQRLKEPRVFWTSTIPILISASDMLSPSLTFLS 570

DB 572 DLSTMPAYNLTQYLQDLNMSLQRLKEPRVFWTSTIPILISASDMLSPSLTFLS 631

QY 571 LLOPFFFCAP 581

DB 632 LLOPFFFCAP 642

RESULT 6

ABP61005

ID ABP61005 standard; protein: 581 AA.

AC ABP61005;

DT 10-SEP-2002 (first entry)

DE Novel human protein. SEQ ID 92.

XX Human; cytostatic; vulnary; antiarteriosclerotic; antiparkinsonian;

XX nootropic; neuroprotective; immunosuppressive; haemostatic;

XX antiinflammatory; cardiac; antilucer; vitruide; antithyroid;

XX cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;

XX wound healing disorders; atherosclerosis; Parkinson's disease;

XX Alzheimer's disease; autoimmune disorder; haematopoietic disorder;

XX inflammation; neoplastic disease; nervous system disorder;

XX cardiovascular disorders; pancreatitis; respiratory disorder;

XX hyperproliferation; systemic autoimmune disease; hyper-immunity;

XX developmental abnormality; gastrointestinal ulceration; neuropathy;

XX haematological disease; metabolic disease; sperm dysfunction;

XX thyroid disorder; hypothyroidism; brain damage; colitis;

XX cone photo-transduction deficiency; neurological disease; stroke;

XX trachea; thymus; lymph node; muscular system; obesity; anorexia;

XX growth abnormality; precocious puberty.

XX Homo sapiens.

XX WO200250105-A1.

XX 27-JUN-2002.  
 PD 17-DEC-2001; 2001WO-US049232.  
 XX 19-DEC-2000; 2000US-0256710P.  
 XX 20-DEC-2000; 2000US-0257048P.  
 PR 09-JAN-2001; 2001US-0260482P.  
 PR 30-JAN-2001; 2001US-0264922P.  
 PR 06-FEB-2001; 2001US-0266797P.  
 PR 19-MAR-2001; 2001US-0276988P.  
 PR 04-APR-2001; 2001US-0281535P.  
 PR 08-MAY-2001; 2001US-0289622P.  
 XX (SMIR) SMITHKLINE BEECHAM CORP.  
 PA (SMIR) SMITHKLINE BEECHAM PLC.  
 PA (GLAXO) GLAXO GROUP LTD.  
 XX Agarwal P, Birkeland M, Cogswell JP, Kadnick KF, Lai Y,  
 PI Martensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q;  
 XX WPI; 2002-508784/54.  
 DR N-PSDB; ABO86170.  
 XX Secreted proteins and polynucleotides useful as vaccines for preventing  
 PT or treating various diseases e.g. cancer, wounds, atherosclerosis,  
 PT Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.  
 XX Claim 1(a); Page 313-314; 335pp; English.  
 CC The invention relates to an isolated polypeptide with signal sequences  
 CC which allow it to be secreted extracellularly or membrane associated. The  
 CC activity of polypeptides of the invention may be described as:  
 CC cytostatic, vulnery, antiarteriosclerotic, antiparkinsonian, nootropic,  
 CC neuroprotective, immunosuppressive, haemostatic, antiinflammatory,  
 CC cardiant, anticulcer, virucide, antihypoid, cerebroprotective, anorectic,  
 CC and metabolic. Polypeptides and polynucleotides of the invention are  
 CC useful in the treatment, or as a vaccine in the prevention of, cancer,  
 CC and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,  
 CC inflammation, neoplastic diseases, nervous system related disorders and  
 CC cardiovascular disorders, pancreatitis, respiratory disorder;  
 CC hyperproliferation, systemic autoimmune disease, hyper-immunity,  
 CC developmental abnormality, gastrointestinal ulceration, neuropathy,  
 CC haematological diseases, metabolic diseases, sperm dysfunction, thyroid  
 CC disorders e.g. hypothyroidism, brain diseases, colitis, cone photo-  
 CC transduction deficiency, neurological diseases, stroke, angiodenesis,  
 CC trachea, thymus, lymph node and muscular system, obesity, anorexia,  
 CC growth abnormalities, and alleviation of precocious puberty. The  
 CC sequences given in records ABP60965-ABP61019 represent novel human  
 CC proteins of the invention  
 XX  
 SO Sequence 581 AA;  
 Query Match 84.7%; Score 2607.5; DB 5; Length 581;  
 Best Local Similarity 91.4%; Pired. No. 1.4e-234;  
 Matches 499; Conservative 7; Mismatches 25; Indels 15; Gaps 3;  
 Oy 12 WCFLLLOPLGHRWGKTPSAEGPQRTLRGLTGMQGVVLGSPVNVNFTLCVPPAP 71  
 Db 14 WAIWVAAP-----TKGPSAEGPQNTLRGLTGMQGVVLGSPVNVNFTLCVPPAP 65  
 Oy 72 PLGSLRFTNPQAPSPMDNRENTSYPNCLQNSEWLLDQMLKVHPKFGVSDCLYLN 131  
 Db 66 PLGSARFTNPQAPSPMDNRENTSYPNCLQNSEWLLDQMLKVHPKFGVSDCLYLN 125  
 Oy 132 IYAPHADTGSULPVLVFPFGAFKTSASIFDSALAAVEDLVVYVYRGLIFGFFTT 191  
 Db 126 IYAPHADTGSULPVLVFPFGAFKTSASIFDSALAAVEDLVVYVYRGLIFGFFTT 185  
 Oy 192 WDOHAPGNMAFKDOYALSWYQKNIFFGGDPSSVTTFGSSAGAISSVSLISPMAGKF 251  
 |||||||

Db 186 WDOHAPGNMAFKDOYALSWYQKNIFFGGDPSSVTTFGSSAGAISSVSLISPMAGKF 245  
 Oy 252 HKAINESGVALIPYLEADHYEKSEDLQVNAHFGGNNAOSEALLRCLRTKPSKELLTTSQ 311  
 Db 246 HKAINESGVALIPYLEADHYEKSEDLQVNAHFGGNNAOSEALLRCLRTKPSKELLTTSQ 305  
 Oy 312 KTKSFTTRVQGAFFPNPDLDSQKAFKAIPISTIGVNNHCEGFLPMKE--APELLSSGN 369  
 Db 306 KTKSFTTRVQGAFFPNPDLDSQKAFKAIPISTIGVNNHCEGFLPMRIILAHMTAPSN 365  
 Oy 370 KSLAL-----HLIONTLHIPPQYLHVANNEYHDDKSLTEIPDSLLDLSGVFFVPVALI 424  
 Db 366 RDALASTAGHFRRHQHIPPQYLHVANNEYHDDKSLTEIPDSLLDLSGVFFVPVALI 425  
 Oy 425 TARYHDGAPVYFFYFFRRRPOCFEDTKPAFYKADHADEVFVFGAFPLKGDVMEFGAT 484  
 Db 426 TARYHDGAPVYFFYFFRRRPOCFEDTKPAFYKADHADEVFVFGAFPLKGDVMEFGAT 485  
 Oy 485 EEEKLISRQMKYKWTAFATGPNNGNDLTPAYNLTEOYLQDLNNSLQRLKEPRVDF 544  
 Db 486 EEEKLISRQMKYKWTAFATGPNNGNDLTPAYNLTEOYLQDLNNSLQRLKEPRVDF 545  
 Oy 545 WTSTIP 550  
 Db 546 WTTGTP 551

RESULT 7  
 ADAS4807.  
 ID ADAS4807 standard; protein; 525 AA.  
 XX  
 AC ADAS4807;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DB Human protein, SEQ ID 2375.  
 XX  
 KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;  
 KW Gene Therapy; human; secretory protein; membrane protein; cancer;  
 KW inflammatory disease; osteoporosis; neurological disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1293569-A2.  
 PD 19-MAR-2003.  
 XX  
 PF 21-MAR-2002; 2002EP-00006586.  
 XX  
 PR 14-SEP-2001; 2001JP-00328381.  
 PR 24-JUN-2002; 2002US-0350435P.  
 XX  
 PA (HELI-) HELIX RES INST.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 PI Isogai T, Sugiyama T, Otsuki T, Makamatsu A, Sato H, Iehli S;  
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,  
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;  
 DR WPI; 2003-395539/38.  
 DR N-PSDB; ADAS3168.  
 XX  
 PT New polynucleotides encoding full-length polypeptides, e.g. secretory  
 PT and/or membrane proteins, useful for developing medicines for diseases in  
 PT which the gene is involved, or as target molecules for gene therapy.  
 XX  
 PS Claim 14; SEQ ID NO 2375; 205pp; English.  
 CC The present invention relates to novel human secretory or membrane  
 CC proteins (ADAS4072-ADAS5710) and their coding sequences (ADAS2433-  
 CC ADAS4071). The coding sequences are useful in the gene therapy of  
 CC diseases caused by abnormalities of the proteins, e.g. cancer,  
 CC inflammatory diseases, osteoporosis or neurological disease.

```

XX      SQ      Sequence 525 AA;
Query Match      84.6%; Score 2606; DB 6; Length 525;
Best Local Similarity 90.9%; Pred. No. 1.7e-234;
Matches 501; Conservative 0; Mismatches 0; Indels 50; Gaps 1;

QY      31 GPSAGGPGQNRRLGWIQKQVTVLSPVNVNFIAGVFAAPPLGSLRFTNPQASPMDNL 90
DB      25 GPSAGGPGQNRRLGWIQKQVTVLSPVNVNFIAGVFAAPPLGSLRFTNPQASPMDNL 84
QY      91 RRAISYPNICLONSEKLLDQMLKXHYKFKGVSEBCLYINLYAPAHADTGSKLPLYVWF 150
DB      85 RRAISYPNICLONSEKLLDQMLKXHYKFKGVSEBCLYINLYAPAHADTGSKLPLYVWF 144
QY      151 PGCAFRTGSASIFDGSALAAVEDLVVVVQYRLGIFGFFTTMDQAHGGMWAKDDVAAALS 210
DB      145 PGCAFRTGSASIFDGSALAAVEDLVVVVQYRLGIFGFFTTMDQAHGGMWAKDDVAAALS 204
QY      211 WYQKNIIEFGDPSVTLIFGESAGAISSVSLILSPMAKGLFKHAKIMESGVAILPYLEAHD 270
DB      205 WYQKNIIEFGDPSVTLIFGESAGAISSVSLILSPMAKGLFKHAKIMESGVAILPYLEAHD 264
QY      271 YEKSEDLQVVAHFCCGNNASDSBALRCLRTKPSKELITLSQTKSFTRVVDGAFPPNEPL 330
DB      265 YEKSEDLQVVAHFCCGNNASDSBALRCLRTKPSKELITLSQTKSFTRVVDGAFPPNEPL 324
QY      331 DLSGKAFAPISIIIVNNHEGCGFLPMKEAPEIISGSKSLALHLIOMILHIPOVYLT 390
DB      325 DLSGKAFAPISIIIVNNHEGCGFLPMKEAPEIISGSKSLALHLIOMILHIPOVYLT 384
QY      391 VANEYFHDGSLTEIRDSLLDLGDFEVVPAALITARYRDGAPVYFYEPHRRPQCFED 450
DB      385 VANEYFHDGSLTEIRDSLLDLGDFEVVPAALITARYRDGAPVYFYEPHRRPQCFED 424
QY      451 TKPAFVADKAHDEVRPFVGCAPFLKGDIVNEEGATEEEKLSRKMKYMATFARTGNPNN 510
DB      425 -----EGATEEEKLSRKMKYMATFARTGNPNN 454
QY      511 DLSLPAVNLTEOYLQDILNMSLQRLKPRVDFMTSTPLILSASDMHSLSTLTF 570
DB      455 DLSLPAVNLTEOYLQDILNMSLQRLKPRVDFMTSTPLILSASDMHSLSTLTF 514
QY      571 LLOPFFFCAP 581
DB      515 LLOPFFFCAP 525

RESULT 8
ABUS4639
ID      ABUS4639 standard; protein; 581 AA.
XX      AC      ABUS4639;
XX      DT      03-JUN-2003 (first entry)
XX      DE      Human NOVX polypeptide #98.
XX      KM      Human; NOVX; metabolic disorder; cardiomyopathy; diabetes; ASD;
XX      KM      hypertension; congenital heart defect; aortic stenosis; valve disease;
XX      KM      atrial septal defect; atriocentric canal defect; ductus arteriosus;
XX      KM      pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD;
XX      KM      tuberosus sclerosis; scleroderma; atherosclerosis; infectious disease;
XX      KM      obesity; anorexia; neurodegenerative disorder; Alzheimer's disease;
XX      KM      Parkinson's disease; immune disorder; haematopoietic disorder;
XX      KM      haemophilia; hypercoagulation; Crohn's disease; cancer.
XX      OS      Homo sapiens.
XX      PN      MO200281498-A2.
XX      PD      17-OCT-2002.
XX

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PF      03-APR-2002; 2002MO-US010780.
XX      PR      03-APR-2001; 2001US-0281086P.
XX      PR      03-APR-2001; 2001US-0281136P.
XX      PR      05-APR-2001; 2001US-0281863P.
XX      PR      05-APR-2001; 2001US-0281906P.
XX      PR      06-APR-2001; 2001US-0282020P.
XX      PR      10-APR-2001; 2001US-0282930P.
XX      PR      10-APR-2001; 2001US-0282934P.
XX      PR      12-APR-2001; 2001US-0283513P.
XX      PR      13-APR-2001; 2001US-0283710P.
XX      PR      17-APR-2001; 2001US-0284234P.
XX      PR      19-APR-2001; 2001US-0285325P.
XX      PR      20-APR-2001; 2001US-0285381P.
XX      PR      20-APR-2001; 2001US-0285609P.
XX      PR      23-APR-2001; 2001US-0285748P.
XX      PR      23-APR-2001; 2001US-0285890P.
XX      PR      24-APR-2001; 2001US-0286068P.
XX      PR      25-APR-2001; 2001US-0286292P.
XX      PR      27-APR-2001; 2001US-0287213P.
XX      PR      02-MAY-2001; 2001US-0288257P.
XX      PR      29-MAY-2001; 2001US-0294164P.
XX      PR      30-MAY-2001; 2001US-0294484P.
XX      PR      18-JUN-2001; 2001US-0296952P.
XX      PR      19-JUN-2001; 2001US-0299237P.
XX      PR      19-JUN-2001; 2001US-0299276P.
XX      PR      12-SEP-2001; 2001US-0318750P.
XX      PR      25-SEP-2001; 2001US-0324800P.
XX      PR      25-SEP-2001; 2001US-0324802P.
XX      PR      27-SEP-2001; 2001US-0325684P.
XX      PR      17-OCT-2001; 2001US-0330143P.
XX      PR      14-NOV-2001; 2001US-0332131P.
XX      PR      14-NOV-2001; 2001US-0332240P.
XX      PR      14-NOV-2001; 2001US-0332779P.
XX      PR      21-NOV-2001; 2001US-0332115P.
XX      PR      04-DEC-2001; 2001US-0337621P.
XX      PR      03-JAN-2002; 2002US-0345783P.
XX      PR      16-JAN-2002; 2002US-0350251P.
XX      PR      02-APR-2002; 2002US-00114270.
XX      PA      (CURA-) CURAGEN CORP.
XX      PI      Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA;
XX      PI      Patuturajan M, Liu X, Gusev VY, Li L, Vernet CM, Zehrhusen BD;
XX      PI      Gorman L, Shenoy SG, Pena CE, Smithson G, Burgess CE, Gerlach V;
XX      PI      Padigaru M, Shinkets RA, Gangoli EA, Taupier RJ, Caeman SJ, Ji W;
XX      PI      Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ;
XX      PI      MacDougall JR, Rothenberg MB, Mazur A, Millet I, Peyman JA;
XX      PI      Ellerman K;
XX      DR      MPI: 2003-046858/04.
XX      DR      N-PSDB; ABX72267.
XX      PT      New isolated NOVX polypeptide useful for treating atherosclerosis,
XX      PT      metabolic disorders, diabetes, obesity, infectious disease, anorexia,
XX      PT      neurodegenerative disorders, Alzheimer's disease and cancer.
XX      PS      Claim 1; Page 303; 666pp; English.
XX      XX
XX      The invention relates to human polypeptides, termed NOVX, and the
XX      CC      polynucleotides encoding them. The polypeptides and polynucleotides are
XX      CC      useful for diagnosing disease, and screening for potential therapeutic
XX      CC      agents. The sequences are useful for treating metabolic disorders,
XX      CC      cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic
XX      CC      stenosis, atrial septal defect (ASD), atriocentric canal defect,
XX      CC      ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular
XX      CC      septal defect (VSD), valve diseases, tuberosus sclerosis, scleroderma,
XX      CC      atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative
XX      CC      disorders, Alzheimer's disease, Parkinson's disease, immune disorders,
XX      CC      haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease
XX      CC      and cancer. Sequences ABUS4542-ABUS4647 represent human NOVX polypeptides
XX      CC      of the invention

```

SQ Sequence 581 AA;

Query Match 84.4%; Score 2597.5; DB 6; Length 581;  
 Best Local Similarity 94.3%; Pred. No. 1.2e-233;  
 Matches 497; Conservative 4; Mismatches 17; Indels 9; Gaps 3;

31 GPSAEGPQRTLRGMVIGKQVTVLGSPPVNVFLGVPFAAPPLGSLRTNQPASPMNDL 90  
 27 GPSAEGPQRTLRGMVIGKQVTVLGSPPVNVFLGVPFAAPPLGSLRTNQPASPMNDL 86  
 91 REATSYPNLCIONSEWLLDQHMVKVHPKFGVSDCLYNTIYAPAHADTGSKLPLYWVF 150  
 87 REATSYPNLCIONSEWLLDQHMVKVHPKFGVSDCLYNTIYAPAHADTGSKLPLYWVF 146  
 151 PGCAFPTGSASIFDGSALAAYEDVLVVVQYRLGIFGFTTWDQAHGNNAPFDQVAAIS 210  
 147 PGCAFPTGSASIFDGSALAAYEDVLVVVQYRLGIFGFTTWDQAHGNNAPFDQVAAIS 206  
 211 WQOKNIEFFGGDPSSVTIFGSAAGISVSSLIISPMKGLFHKAINESGVAILIPLYEAHD 270  
 207 WQOKNIEFFGGDPSSVTIFGSAAGISVSSLIISPMKGLFHKAINESGVAILIPLYEAHD 266  
 271 YEKSEDLQVNAHFCGNNASDSEALRLCLRTKPSKELLITLSQKTSFTRVVDGAFPPNEBL 330  
 267 YEKSEDLQVNAHFCGNNASDSEALRLCLRTKPSKELLITLSQKTSFTRVVDGAFPPNEBL 326  
 331 DLSQKAFKAIPISTIIGVNNHCEGFLPMKE--APELLGSKNSKSLAL----HLIQNLIHI 383  
 327 DLSQKAFKAIPISTIIGVNNHCEGFLPMKE--APELLGSKNSKSLAL----HLIQNLIHI 384  
 384 PPOYLHVANEYFHDGSLTEIRDSLLDLGDFVFPVPAALITARYHDAAGAPVYEFERH 443  
 385 PPOYLHVANEYFHDGSLTEIRDSLLDLGDFVFPVPAALITARYHDAAGAPVYEFERH 444  
 444 RPQCFEDTKPAFYKADHAEVRFVFGAFLKGDIVMEGATTEELLSRKKMKWTATPAR 503  
 445 RPQCFEDTKPAFYKADHAEVRFVFGAFLKGDIVMEGATTEELLSRKKMKWTATPAR 504  
 504 TGNPNNDLSLMPAYNLTEQYIQLDLNNSLQRLKEPRVDFTSTIP 550  
 505 TGNPNNDLSLMPAYNLTEQYIQLDLNNSLQRLKEPRVDFTSTIP 551

RESULT 9

ADRI9663 standard; protein; 618 AA.

AC ADR19663;

DT 07-OCT-2004 (first entry)

DE Human drug metabolizing enzyme (DME)-2 protein sequence.

KW drug metabolizing enzyme; DME; cytostatic; immunosuppressive;  
 KW antiinflammatory; endocrine; ophthalmological; gastrointestinal;  
 KW hepatotropic; cancer; cell proliferative disorder; autoimmune disorder;  
 KW inflammatory disorder; endocrine disorder; eye disorder;  
 KW gastrointestinal disorder; liver disorder; metabolic disorder; enzyme;  
 KW human.

OS Homo sapiens.

PN MO200226988-A2.

PD 04-APR-2002.

PF 28-SEP-2001; 2001MO-US030662.

PR 29-SEP-2000; 2000US-0236947P.

PR 06-OCT-2000; 2000US-0238664P.

PR 20-OCT-2000; 2000US-0242323P.

PR 09-NOV-2000; 2000US-0247581P.

PR 16-NOV-2000; 2000US-0249519P.

PR 22-NOV-2000; 2000US-0252834P.  
 PR 30-NOV-2000; 2000US-0250567P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.

PI Azinza Y, Baughin MR, Borowsky ML, Ding L, Duggan BM,  
 PI Elliott VS, Gandhi AR, Griffin JA, Hatfield AJ, Ison CH, Khan PA,  
 PI Lal P, Lee EA, Lu DM, Nguyen DB, Arvizu C, Policky JL, Ramkumar J,  
 PI Ring HZ, Sanjamaal MS, Tang YT, Tribouley CW, Nardinder WK,  
 PI Walsh RT, Warren BA, Xu Y, Yang J, Yao MG, Yue H,  
 DR WPI; 2002-362498/39.  
 DR N-PSDB; ADR19681.

PT Human drug metabolizing enzymes, useful in the diagnosis and treatment of  
 PT disorders associated with aberrant (DME) activity, e.g., cancer and  
 PT autoimmune disorders.

PS Claim 1; SEQ ID NO 2; 142pp; English.

CC This invention relates to novel drug metabolizing enzymes (DME) and the  
 CC nucleotide sequences which encode them. The invention may be useful for  
 CC the development of compounds with a cytostatic, immunosuppressive,  
 CC antiinflammatory, endocrine, ophthalmological, gastrointestinal or  
 CC hepatotropic activity acting as an agonist or antagonist of drug  
 CC metabolizing enzyme activity. The invention may be used in the diagnosis  
 CC and treatment of disorders associated with decreased or increased  
 CC expression or activity of drug metabolizing enzymes. Such disorders  
 CC include cancer, cell proliferative disorders, autoimmune/inflammatory,  
 CC endocrine, eye, gastrointestinal (including liver disorders),  
 CC metabolic disorders. The present sequence is that of a human drug  
 CC metabolizing enzyme (DME) of the invention. Note: This sequence did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from EPO.

SQ Sequence 618 AA;

Query Match 84.1%; Score 2588.5; DB 5; Length 618;  
 Best Local Similarity 94.4%; Pred. No. 9.6e-233;  
 Matches 491; Conservative 1; Mismatches 5; Indels 23; Gaps 1;

31 GPSAEGPQRTLRGMVIGKQVTVLGSPPVNVFLGVPFAAPPLGSLRTNQPASPMNDL 90  
 92 GPSAEGPQRTLRGMVIGKQVTVLGSPPVNVFLGVPFAAPPLGSLRTNQPASPMNDL 151  
 91 REATSYPNLCIONSEWLLDQHMVKVHPKFGVSDCLYNTIYAPAHADTGSKLPLYWVF 150  
 152 REATSYPNLCIONSEWLLDQHMVKVHPKFGVSDCLYNTIYAPAHADTGSKLPLYWVF 211  
 151 PGCAFPTGSASIFDGSALAAYEDVLVVVQYRLGIFGFTTWDQAHGNNAPFDQVAAIS 210  
 212 PGCAFPTGSASIFDGSALAAYEDVLVVVQYRLGIFGFTTWDQAHGNNAPFDQVAAIS 271  
 211 WQOKNIEFFGGDPSSVTIFGSAAGISVSSLIISPMKGLFHKAINESGVAILIPLYEAHD 270  
 272 WQOKNIEFFGGDPSSVTIFGSAAGISVSSLIISPMKGLFHKAINESGVAILIPLYEAHD 331  
 271 YEKSEDLQVNAHFCGNNASDSEALRLCLRTKPSKELLITLSQKTSFTRVVDGAFPPNEBL 330  
 332 YEKSEDLQVNAHFCGNNASDSEALRLCLRTKPSKELLITLSQKTSFTRVVDGAFPPNEBL 391  
 331 DLSQKAFKAIPISTIIGVNNHCEGFLPMKEAPPLISGNSKSLALHLIQNLIHIPLYEHL 390  
 392 DLSQKAFKAIPISTIIGVNNHCEGFLPM-----HIPOYLHL 428  
 391 VANEYFHDGSLTEIRDSLLDLGDFVFPVPAALITARYHDAAGAPVYEFERHPOCED 450  
 429 VANEYFHDGSLTEIRDSLLDLGDFVFPVPAALITARYHDAAGAPVYEFERHPOCED 488  
 451 TKPAFYKADHAEVRFVFGAFLKGDIVMEGATTEELLSRKKMKWTATPARIGNNGN 510  
 489 TKPAFYKADHAEVRFVFGAFLKGDIVMEGATTEELLSRKKMKWTATPARIGNNGN 548



QY 511 DLSLTPAYNLTEQYIQLDLNMSLGGRLKEPRVDFTSTIP 550  
 DB 549 DLSLTPAYNLTEQYIQLDLNMSLGGRLKEPRVDFTSTIP 588

## RESULT 10

ADBE4065  
 ID ADBE4065 standard; protein; 469 AA.

AC ADBE4065;

DT 04-DEC-2003 (first entry)

DE Human protein encoded by clone BRAHM20021910.

KM Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;  
 cell regeneration; membrane protein; signal transduction-related protein;  
 transcription-related protein; osteoporosis; neurological disease;  
 cancer; tumour.

OS Homo sapiens.

XX EPI308459-A2.

XX 07-MAY-2003.

XX 28-MAR-2002; 2002EP-00007401.

XX 05-NOV-2001; 2001JP-00379298.

XX 25-JAN-2002; 2002US-00350978.

XX (HELI-) HELIX RES INST.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Isogai T, Sugiyama T, Otsuki T, Makamatsu A, Sato H, Ishii S,  
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,  
 PI Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuho Y;

XX MPI; 2003-450961/43.

XX N-PSDB; ADBE2095.

PT New polynucleotides and polypeptides, useful for developing a diagnostic  
 marker or medicines for regulation of their expression and activity, or  
 as targets of gene therapy.

PS Claim 1; Page; 222pp; English.

CC The invention discloses a polynucleotide comprising a sequence selected  
 CC from 1970 fully defined nucleotide sequences which encode novel  
 CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide  
 CC or its partial peptide, an antibody binding to the polypeptide or peptide  
 CC of the polynucleotide, immunologically assaying the polypeptide or  
 CC peptide of the polynucleotide by contacting the polypeptide or peptide  
 CC with the antibody of the encoded protein, and observing the binding  
 CC between the two, a transformant carrying the polynucleotide in an  
 CC expressible manner and an antisense polynucleotide. The oligonucleotide  
 CC is useful as a primer for synthesizing the polynucleotide, or as a probe  
 CC for detecting the polynucleotide. The polynucleotides and encoded  
 CC proteins are useful as pharmaceutical agents and many disease-related  
 CC genes may be included in them, for developing a diagnostic marker or  
 CC medicines for regulation of their expression and activity, or as targets  
 CC of gene therapy. The genes are involved in tissue and/or cell  
 CC regeneration. Membrane proteins, signal transduction-related proteins,  
 CC transcription-related proteins, disease-related proteins and genes  
 CC encoding them can be used as indicators for diseases (e.g. osteoporosis,  
 CC neurological diseases, cancer, tumours). The cDNA may be used to regulate  
 CC the activity or expression of the encoded protein to treat diseases. The  
 CC sequence presented is a protein of the invention. Note: Some of the  
 CC sequence data for this patent is not represented in the printed  
 CC specification, but is based on sequence information supplied by the  
 CC European Patent Office.

XX Sequence 469 AA;

Query Match 79.7%; Score 2454; DB 7; Length 469;  
 Best Local Similarity 99.6%; Pred. No. 2.4e-220;  
 Matches 467; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 113 MLKHYHFFEGVSEDCLYNITYAPAHADGSKLPVLVWPPGGAFTKGSITFDGSLAYE 172  
 DB 1 MLKHYHFFEGVSEDCLYNITYAPAHADGSKLPVLVWPPGGAFTKGSITFDGSLAYE 60  
 QY 173 DVLVWVVOYRLGIRGFPTTMDQHAPGNMAFPDQVAAALSMVQNIFFPGDSSVTIFGES 232  
 DB 61 DVLVWVVOYRLGIRGFPTTMDQHAPGNMAFPDQVAAALSMVQNIFFPGDSSVTIFGES 120  
 QY 223 AGAIVSSSLISPMAGLPHKAIMESGVAIIPYLEANDYKSEDLQVVAHFCGNNAADSE 292  
 DB 121 AGAIVSSSLISPMAGLPHKAIMESGVAIIPYLEANDYKSEDLQVVAHFCGNNAADSE 180  
 QY 293 ALLRCLRTKPSKELLTTSQKTSFTRVVDGAFPPHPEPDLISQKAFKAIPISTIGVNSHC 352  
 DB 181 ALLRCLRTKPSKELLTTSQKTSFTRVVDGAFPPHPEPDLISQKAFKAIPISTIGVNSHC 240  
 QY 353 GFLPMPKAPETLISGNSKSLALHLIQLNLIHPQYLHLVANEYFHDKSLTEIRDSLDL 412  
 DB 241 GFLPMPKAPETLISGNSKSLALHLIQLNLIHPQYLHLVANEYFHDKSLTEIRDSLDL 300  
 QY 413 LGDVFVVPALITARYHRDAGAPVYFYEFRHRPOCFEDTKPAFYKADHAEVRFVGGAF 472  
 DB 301 LGDVFVVPALITARYHRDAGAPVYFYEFRHRPOCFEDTKPAFYKADHAEVRFVGGAF 360  
 QY 473 LKGDIVMEGATTEBKSLSRQMKYKWPARTGNPNQDLSLMPAYNLTEQYIQLDLNMS 532  
 DB 361 LKGDIVMEGATTEBKSLSRQMKYKWPARTGNPNQDLSLMPAYNLTEQYIQLDLNMS 420  
 QY 533 LGORLKEPRVDFTSTIPLILASDMLHSPSLSTPLSLQPPFFPCAP 581  
 DB 421 LGORLKEPRVDFTSTIPLILASDMLHSPSLSTPLSLQPPFFPCAP 469

## RESULT 11

ADFS0145  
 ID ADFS0145 standard; protein; 542 AA.

XX ADFS0145;

DT 12-FEB-2004 (first entry)

DE Cat cauxin protein SEQ ID NO:2.

KM cat; cauxin; cat kidney disease marker; kidney disease.

OS Felis catus.

XX JP2003250575-A.

XX 09-SEP-2003.

XX 04-MAR-2002; 2002JP-00057908.

XX 04-MAR-2002; 2002JP-00057908.

XX (TOHO-) TOHOKU TECHNOARCH KK.

XX MPI; 2004-002277/01.

XX N-PSDB; ADFS0144.

PT Novel cauxin protein or its salt, useful as a cat kidney disease marker,  
 and for diagnosing cat kidney disease.

PS Claim 3; SEQ ID NO 2; 33pp; Japanese.

CC The present sequence represents a cat cauxin protein (I) or its salt,  
 CC which is cat kidney disease marker. Also described: (1) a partial peptide  
 CC (II) of (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector

CC (IV) comprising (III); (4) a transformed host (V) comprising (III) or  
 CC (IV); (5) producing (I) or (II) by culturing (V); (6) an antibody (VI)  
 CC which couples specifically with (I) or (II); (7) diagnosing cat kidney  
 CC disease which involves measuring (I) quantitatively, and where reduction  
 CC of amount of (I) indicates presence of the disease; (8) a cat kidney  
 CC disease diagnostic agent comprising (I) labelling agent, a reagent which  
 CC measures the biological activity of urinary (I) or (VI); and (9) a cauxin  
 CC detection kit which measures cauxin in a test sample. (I) is useful as a  
 CC cat kidney disease marker and (VI) is useful for diagnosing cat kidney  
 CC disease. (I) enables detection of cat kidney disease simply and  
 CC correctly. (I) provides an early marker for the disease, and replaces  
 CC complicated diagnostic methods such as X-ray imaging, ultrasonic imaging,  
 CC blood testing.

CC Sequence 542 AA;

Query Match 64.5%; Score 1985; DB 8; Length 542;  
 Best Local Similarity 71.7%; Pred. No. 2.4e-176;  
 Matches 373; Conservative 60; Mismatches 85; Indels 2; Gaps 2;

QY 31 GPSAEGQRTNRLGMLGKQVTVLGSFVNVNVLGVFPAAPLGLRFTNPQASPMNDL 90  
 DB 22 GPADABVSTRSLGWRGKQTVLGSFVNVNVLGVFPAAPLGLRFTNPQASPMNDL 90  
 QY 91 REATSPNLCQNSEWLLDQHLKYHPRKGVSEDCLYNTYAPAHADTGSKLPVLWF 150  
 DB 82 RNATSPNLCQNSEWLLDQHLKYHPRKGVSEDCLYNTYAPAHADTGSKLPVLWF 150  
 QY 151 PGAFPTGSASIFDGSALAAEDVTVVVOYRLGIFGFPTTWDQAHAGNMAFKDQVALS 210  
 DB 142 PGAFPTGSASIFDGSALAAEDVTVVVOYRLGIFGFPTTWDQAHAGNMAFKDQVALS 210  
 QY 211 WQKNIEFGDPSVTIFGSAGAISSVSLISPMAGLFHKAIMESGVAIIPLYL-EAH 269  
 DB 202 WVRDNIIEFGDPSVTIFGSAGAISSVSLISPMAGLFHKAIMESGVAIIPLYL-EAH 269  
 QY 270 DYKESDDQVNAHFCGNASDSEALRLCLRTKPSKELLTLOKTSFTRVVDGAFPPNP 329  
 DB 262 GDERKDDQVNAHFCGNASDSEALRLCLRTKPSKELLTLOKTSFTRVVDGAFPPNP 329  
 QY 330 LDLSQKAFKAIPISTIGVNNHECGFLPMKEAPBIIISGNSKSLALHLIQNTLHIPQYLH 389  
 DB 322 VALLTQKAFNSVPSIIGVNNHECAFLL-STEFSEIIIGGNSRSLALVHTFLNIPQYLH 380  
 QY 390 LVANEYFHDKSLTEIRDSLLDLGDFVFPVPAITARYHRDAGAPVYFEFRHRPQCE 449  
 DB 381 LVADHYFYNKHSPEIRDSFLDLGDFVFPVPAITARYHRDAGAPVYFEFRHRPQCE 440  
 QY 450 DTKPAFYKADHAEVRFVFGAFLKGDIVFEGATEEBEKLRSKMKWATPARTGNPNG 509  
 DB 441 DTKPAFYKADHAEVRFVFGAFLKGDIVFEGATEEBEKLRSKMKWATPARTGNPNG 500  
 QY 510 NDLSLWPAVNLTEOYLQDLNMSLGRLKEPRVDFTSTI 549  
 DB 501 EGVPLWPAVNLTEOYLQDLNMSLGRLKEPRVDFTSTI 540

RESULT 12  
 ADF50147  
 ID ADF50147 standard; protein; 542 AA.  
 AC ADF50147;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Cat cauxin protein SEQ ID NO:4.  
 XX  
 KW cat; cauxin; cat kidney disease marker; kidney disease.  
 XX  
 OS Felis catus.  
 XX  
 FN JP2003250575-A.  
 XX

PD 09-SEP-2003.  
 XX  
 XX 04-MAR-2002; 2002JP-00057908.  
 PF  
 XX 04-MAR-2002; 2002JP-00057908.  
 PR  
 XX (TOHO-) TOHOKU TECHNOARCH KK.  
 XX  
 XX WPI; 2004-002277/01.  
 DR  
 XX N-PSDB; ADF50146.  
 PT Novel cauxin protein or its salt, useful as a cat kidney disease marker,  
 PT and for diagnosing cat kidney disease.  
 PS Disclosure; SEQ ID NO 4; 33pp; Japanese.

The present sequence represents a cat cauxin protein (I) or its salt,  
 CC which is cat kidney disease marker. Also described: (1) a partial peptide  
 CC (II) of (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector  
 CC (IV) comprising (III); (4) a transformed host (V) comprising (III) or  
 CC (IV); (5) producing (I) or (II) by culturing (V); (6) an antibody (VI)  
 CC which couples specifically with (I) or (II); (7) diagnosing cat kidney  
 CC disease which involves measuring (I) quantitatively, and where reduction  
 CC of amount of (I) indicates presence of the disease; (8) a cat kidney  
 CC disease diagnostic agent comprising (I) labelling agent, a reagent which  
 CC measures the biological activity of urinary (I) or (VI); and (9) a cauxin  
 CC detection kit which measures cauxin in a test sample. (I) is useful as a  
 CC cat kidney disease marker and (VI) is useful for diagnosing cat kidney  
 CC disease. (I) enables detection of cat kidney disease simply and  
 CC correctly. (I) provides an early marker for the disease, and replaces  
 CC complicated diagnostic methods such as X-ray imaging, ultrasonic imaging,  
 CC blood testing.

Sequence 542 AA;

Query Match 64.5%; Score 1985; DB 8; Length 542;  
 Best Local Similarity 71.7%; Pred. No. 2.4e-176;  
 Matches 373; Conservative 60; Mismatches 85; Indels 2; Gaps 2;

QY 31 GPSAEGQRTNRLGMLGKQVTVLGSFVNVNVLGVFPAAPLGLRFTNPQASPMNDL 90  
 DB 22 GPADABVSTRSLGWRGKQTVLGSFVNVNVLGVFPAAPLGLRFTNPQASPMNDL 90  
 QY 91 REATSPNLCQNSEWLLDQHLKYHPRKGVSEDCLYNTYAPAHADTGSKLPVLWF 150  
 DB 82 RNATSPNLCQNSEWLLDQHLKYHPRKGVSEDCLYNTYAPAHADTGSKLPVLWF 150  
 QY 151 PGAFPTGSASIFDGSALAAEDVTVVVOYRLGIFGFPTTWDQAHAGNMAFKDQVALS 210  
 DB 142 PGAFPTGSASIFDGSALAAEDVTVVVOYRLGIFGFPTTWDQAHAGNMAFKDQVALS 210  
 QY 211 WQKNIEFGDPSVTIFGSAGAISSVSLISPMAGLFHKAIMESGVAIIPLYL-EAH 269  
 DB 202 WVRDNIIEFGDPSVTIFGSAGAISSVSLISPMAGLFHKAIMESGVAIIPLYL-EAH 269  
 QY 270 DYKESDDQVNAHFCGNASDSEALRLCLRTKPSKELLTLOKTSFTRVVDGAFPPNP 329  
 DB 262 GDERKDDQVNAHFCGNASDSEALRLCLRTKPSKELLTLOKTSFTRVVDGAFPPNP 329  
 QY 330 LDLSQKAFKAIPISTIGVNNHECGFLPMKEAPBIIISGNSKSLALHLIQNTLHIPQYLH 389  
 DB 322 VALLTQKAFNSVPSIIGVNNHECAFLL-STEFSEIIIGGNSRSLALVHTFLNIPQYLH 380  
 QY 390 LVANEYFHDKSLTEIRDSLLDLGDFVFPVPAITARYHRDAGAPVYFEFRHRPQCE 449  
 DB 381 LVADHYFYNKHSPEIRDSFLDLGDFVFPVPAITARYHRDAGAPVYFEFRHRPQCE 440  
 QY 450 DTKPAFYKADHAEVRFVFGAFLKGDIVFEGATEEBEKLRSKMKWATPARTGNPNG 509  
 DB 441 DTKPAFYKADHAEVRFVFGAFLKGDIVFEGATEEBEKLRSKMKWATPARTGNPNG 500  
 QY 510 NDLSLWPAVNLTEOYLQDLNMSLGRLKEPRVDFTSTI 549  
 DB 501 EGVPLWPAVNLTEOYLQDLNMSLGRLKEPRVDFTSTI 540



Db 501 EGVPLMPAYTQSEQYLKLDLSVSGQKKEQVEFMNNTI 540

RESULT 13

ABP61006 ID ABP61006 standard; protein; 356 AA.  
 XX  
 AC ABP61006;  
 XX  
 DT 10-SEP-2002 (first entry)  
 XX  
 DE Novel human protein. SEQ ID 93.  
 XX  
 KW Human; cytosolic; vulnary; antiarteriosclerotic; antiparkinsonian;  
 KW neurologic; neuroprotective; immunosuppressive; haemostatic;  
 KW antiinflammatory; cardiac; antitumor; virucide; antithyroid;  
 KW cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;  
 KW wound healing disorder; atherosclerosis; parkinson's disease;  
 KW Alzheimer's disease; autoimmune disorder; haematopoietic disorder;  
 KW inflammation; neoplastic disease; nervous system disorder;  
 KW cardiovascular disorders; pancreatic; respiratory disorder;  
 KW hyperproliferation; systemic autoimmune disease; hyper-immunity;  
 KW developmental abnormality; gastrointestinal ulceration; neuropathy;  
 KW haematological disease; metabolic disease; sperm dysfunction;  
 KW thyroid disorder; hypothyroidism; brain damage; colitis;  
 KW cone photo- transduction deficiency; neurological disease; stroke;  
 KW angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;  
 KW trachea; thymus; lymph node; muscular system; obesity; anorexia;  
 KW growth abnormality; precocious puberty.  
 XX  
 OS Homo sapiens.  
 PN W0200250105-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 17-DEC-2001; 2001WO-US049232.  
 XX  
 PR 19-DEC-2000; 2000US-0256710P.  
 PR 20-DEC-2000; 2000US-0257048P.  
 PR 09-JAN-2001; 2001US-0260482P.  
 PR 30-JAN-2001; 2001US-0264922P.  
 PR 06-FEB-2001; 2001US-0266797P.  
 PR 19-MAR-2001; 2001US-0276988P.  
 PR 04-APR-2001; 2001US-0281535P.  
 PR 08-MAY-2001; 2001US-0289622P.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA (GLAX ) GLAXO GROUP LTD.  
 XX  
 PI Agarwal P, Birkeland M, Cogswell JP, Kabnick KF, Lai Y;  
 PI Mathensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q;  
 XX  
 DR WPI: 2002-508784/54.  
 XX  
 N-PSDB; ABQ66171.  
 XX  
 PT Secreted proteins and polynucleotides useful as vaccines for preventing  
 PT or treating various diseases e.g. cancer, wounds, atherosclerosis,  
 PT Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.  
 XX  
 PS Claim 1(a); Page 315; 335pp; English.  
 XX  
 CC The invention relates to an isolated polypeptide with signal sequences  
 CC which allow it to be secreted extracellularly or membrane associated. The  
 CC activity of polypeptides of the invention may be described as,  
 CC cytosolic, vulnary, antiarteriosclerotic, antiparkinsonian, neurologic,  
 CC neuroprotective, immunosuppressive, haemostatic, antiinflammatory,  
 CC cardiac, antitumor, virucide, antithyroid, cerebroprotective, anorectic,  
 CC and metabolic. Polypeptides and polynucleotides of the invention are  
 CC useful in the treatment, or as a vaccine in the prevention of, cancer,  
 CC wound healing disorders, infection, atherosclerosis, parkinson's disease  
 CC and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,

CC inflammation, neoplastic diseases, nervous system related disorders and  
 CC cardiovascular disorders, pancreatitis, respiratory disorder,  
 CC hyperproliferation, systemic autoimmune disease, hyper-immunity,  
 CC developmental abnormality, gastrointestinal ulceration, neuropathy,  
 CC haematological diseases, metabolic diseases, sperm dysfunction, thyroid  
 CC disorders e.g. hypothyroidism, brain damages, colitis, cone photo-  
 CC transduction deficiency, neurological diseases, stroke, angiogenesis,  
 CC ovulation disorders, diseases in the spinal cord, thyroid gland, heart,  
 CC trachea, thymus, lymph node and muscular system, obesity, anorexia,  
 CC growth abnormalities, and alleviation of precocious puberty. The  
 CC sequences given in record ABP60965-ABP61019 represent novel human  
 CC proteins of the invention  
 CC  
 XX

Sequence 356 AA;

Query Match 57.8%; Score 1780; DB 5; Length 356;  
 Best Local Similarity 100.0%; Pred. No. 2e-157;  
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 242 ILSPMAKGLFHKAIMESGVAIIPYLEADHYEKSEDLQVVAHFCGNASDSEALLRLCRLTK 301  
 Db 17 ILSPMAKGLFHKAIMESGVAIIPYLEADHYEKSEDLQVVAHFCGNASDSEALLRLCRLTK 76  
 Qy 302 PSKELLTLGQTKTSFTVVDGAFPPNRPDLDSQAKAKAIPTIIGVNNHCGFLLPMKEA 361  
 Db 77 PSKELLTLGQTKTSFTVVDGAFPPNRPDLDSQAKAKAIPTIIGVNNHCGFLLPMKEA 136  
 Qy 362 PEILSGNSKSLALHLINILHIPPQYALVANEVFNHKSILTEIRDSLILDLGVPFVVP 421  
 Db 137 PEILSGNSKSLALHLINILHIPPQYALVANEVFNHKSILTEIRDSLILDLGVPFVVP 196  
 Qy 422 ALITARYRDAGAVPYEFERHRRPQCEFDTPAFVKAHDADVAFVGAFLLKGDIVME 481  
 Db 197 ALITARYRDAGAVPYEFERHRRPQCEFDTPAFVKAHDADVAFVGAFLLKGDIVME 256  
 Qy 482 GATEEEKLISRKMKYATATPRTGNPNDLSLMPAYNLTEQYQLDNLNLSGRLKEPR 541  
 Db 257 GATEEEKLISRKMKYATATPRTGNPNDLSLMPAYNLTEQYQLDNLNLSGRLKEPR 316  
 Qy 542 VDFWSTITPLILASDMLHSPLSLTFSLLOPFPPFCAP 581  
 Db 317 VDFWSTITPLILASDMLHSPLSLTFSLLOPFPPFCAP 356

RESULT 14

AAE20911 ID AAE20911 standard; protein; 561 AA.  
 XX  
 AC AAE20911;  
 XX  
 DT 01-JUL-2002 (first entry)  
 XX  
 DE Rat carboxylesterase-like enzyme protein.  
 XX  
 KW Rat; carboxylesterase-like enzyme; organophosphorus intoxication;  
 KW osteopathic; gene therapy; osteoporosis; antisense therapy; cytosolic;  
 KW detoxifying agent; Paget's disease; bone implant degradation; cancer;  
 KW dental implant; enzyme; gene expression.  
 XX  
 OS Rattus sp.  
 XX  
 PN W0200206454-A2.  
 XX  
 PD 24-JAN-2002.  
 XX  
 PF 10-JUL-2001; 2001WO-EP007919.  
 XX  
 PR 17-JUL-2000; 2000US-0218564P.  
 XX  
 PA (FARB ) BAYER AG.  
 XX  
 PI Xiao Y;  
 XX

31 Mismatches 168; Indels 24; Gaps 8;

Query Match	39.9%	Score 1230;	DB 3;	Length 549;
Best Local Similarity	46.7%	Pred. No. 1.2e-105;		
Matches 248;	Conservative 91;	Mismatches 168;	Indels 24;	Gaps
QY	31	GPSAEGPQRNRILGICQKQVTVIGSGVPPVNVFGLGVFAAPLGISLRFPNPPASPMWNL	90	8

Db 16 GODSASPIRITHTGQVLSLVHVKGANAGVOTFLGI PPAKPPGLRPAPEPPESWGV 75  
QY 91 REATSYPNLCTON-----SEWLLDQMLKVHYPKFVSEBDCLYNTIYAPAHADTGSKL 145  
Db 76 RDGTHPAMCQDLTAVERSEFL-----SQPNMTFSDSMEBDCLYISTYTPAHSHESNLP 131  
QY 146 VLWVFPFGAFKTGSASIFDGSALAAVEDVLVWVVOYRLGIFGFTTWDQHAPEGNAFKDQ 205  
Db 132 VMVMIHGALVFGWASLYDGSWLALENVWVVIIOYRLGVLGFFSTGDKHATGNWGYLDQ 191  
QY 206 VAAISWVQKNIIEFPGDSSVTITFESAGAISVSSLISPMKGLFHKAIMESGVAIIPY 265  
Db 192 VAALRWQONIAHFGGNPDRAVTITFESAGTSVSSLVSPISQGLFHGAIMESGVALLPG 251  
QY 266 LEADYEKSEDL--QVNAHFCGNNADESEALLRCLRTKPKSKELTLSQXTKSFTFVVDGA 323  
Db 252 LIA-----SSADVISTVVAANTLACQDVDESEALVGCIRGKSKEIILAINKPFKMIPEGVDGV 307  
QY 324 FFPNEPDLDSQAKFKAIPSIIGVNNHECGFLP---MKAPEIISGSNKSALHL1QN 379  
Db 308 FLPRHPQELASADRPVPSIVGVNNNEFGWILIPKWRIVDTQKEMDREASQALQKMLT 367  
QY 380 ILHIPPQYLHVAANEYFHDKSLTEIRDSLDDLGDVFPVVPALITARYHRDAGAPYFY 439  
Db 368 LLMLEPTFTGDLIREEYIGDNGDPQTLQAQFQEMMADSMFVIPALQVAHF-QCSRAPVYFY 426  
QY 440 EFRHRPQCFEDTKPAFVAKADHADEVRFVFGGAFLLKGDIVMEFEGATEEEKLSRKKMKYMA 499  
Db 427 EFOHOPSWLKNIRPPHMKADHGDLELPVF-RSFFGANYIKF---TEEEQLSRKKMKYMA 482  
QY 500 TFARTGNPNNGDLSLMPAYNLTEOYLQDLNMSLGOQLKEPRVDFWTSTIP 550  
Db 483 NFAANGNPNNGSLPWHPLFDQEBQYLQNLQPAVGRAKKAHRLQFWKKALP 533

Search completed: June 16, 2005, 20:41:52  
Job time : 173 secs



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OM protein - protein search, using SW model

Run on: June 16, 2005, 20:28:44 ; Search time 43 Seconds  
(without alignments)  
1300.045 Million cell updates/sec

Title: US-10-674-636-2  
Perfect score: 3079  
Sequence: 1 MPQGLTSSASQWCFLLIQP.....PLSLTFLSLIQPFPPFCAP 581

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1298.5	42.2	557	2	A47162 thiolesterase B (B
2	1231.5	40.0	532	2	A43439 60K esterase (EC 3
3	1230	39.9	559	1	UC5408 carboxylesterase (
4	1199	38.9	561	2	S47655 carboxylesterase (
5	1186.5	38.5	554	1	S34607 carboxylesterase (
6	1163	37.8	554	2	A39060 carboxylesterase (
7	1162.5	37.8	566	2	S19307 carboxylesterase (
8	1144	37.2	549	2	UK0054 carboxylesterase (
9	1140	37.0	567	1	A41010 carboxylesterase (
10	1139	37.0	561	2	S62788 carboxylesterase (
11	1138.5	37.0	562	2	A55281 carboxylesterase (
12	1136	36.9	540	2	A31584 carboxylesterase (
13	1129.5	36.7	561	2	S71597 carboxylesterase (
14	1123	36.5	561	2	UC2447 carboxylesterase (
15	1121.5	36.4	565	2	S10367 carboxylesterase (
16	1034.5	33.6	539	2	A29923 carboxylesterase (
17	777	25.2	596	1	ACRYE acetylcholinestera
18	764.5	24.8	614	2	A39256 acetylcholinestera
19	763	24.8	614	2	UH0314 acetylcholinestera
20	756	24.6	599	1	A38868 acetylcholinestera
21	754	24.5	614	2	UH0811 acetylcholinestera
22	752	24.4	602	1	ACHU acetylcholinestera
23	740	24.0	603	2	S70849 acetylcholinestera
24	732	23.8	581	2	C39768 acetylcholinestera
25	726.5	23.6	584	2	S48724 acetylcholinestera
26	710.5	23.1	583	2	S10712 acetylcholinestera
27	692.5	22.5	620	2	A54413 acetylcholinestera
28	660	21.4	745	2	S13586 triacylglycerol 11
29	658.5	21.4	489	2	B69680 para-nitrobenzyl e

30	643.5	20.9	597	2	A33668 sterol esterase (B
31	633.5	20.6	599	2	A57701 sterol esterase (B
32	627.5	20.4	664	2	UC7990 acetylcholinestera
33	618	20.1	612	2	A34967 sterol esterase (B
34	594.5	19.3	691	2	JE0150 acetylcholinestera
35	593	19.3	550	1	A34576 crystal protein pr
36	586	19.0	767	2	S47639 acetylcholinestera
37	581.5	18.9	746	2	A25363 acetylcholinestera
38	575	18.7	540	2	S51043 carboxylesterase (
39	572.5	18.6	602	2	T37254 acetylcholinestera
40	570.5	18.5	637	2	S66236 acetylcholinestera
41	569.5	18.5	554	2	T31783 hypothetical prote
42	569.5	18.5	557	2	A56690 esterase - Caenorh
43	562.5	18.3	545	2	A89046 protein B0238.1 (i
44	557.5	18.1	593	1	S25062 triacylglycerol 11
45	551	17.9	562	2	S27782 esterase precursor

ALIGNMENTS

RESULT 1

thiolesterase B (EC 3.-.-.-) precursor - mallard  
C/Species: Anas platyrhynchos (mallard)  
C/Date: 05-May-1995 #sequence\_revision 05-May-1995 #text\_change 09-Jul-2004  
C/Accession: A47162  
R/Hwang, C.S.; Koliatukudy, P.E.  
J. Biol. Chem. 268, 14278-14284, 1993  
A/Title: Molecular cloning and sequencing of thioesterase B cDNA and stimulation of expt  
A/Reference number: A47162; MUID:93300823; PMID:8314791  
A/Accession: A47162  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-557 <HNA>  
A/Cross-references: UNIPROT:Q04791; GB:L05493; NID:9213100; PIDN:AAA49223.1; PID:9213101  
C/Superfamily: cholinesterase; cholinesterase homology  
C/Keywords: hydrolase  
F/56-545/Domain: cholinesterase homology <CHE>

Query Match	42.2%	Score 1298.5	DB 2	Length 557
Best Local Similarity	48.4%	Pred. No. 4.1e-94		
Matches 265	Conservative 177	Mismatches 177	Indels 27	Gaps 8
QY	30	TGPEAGPQNTNRGWIQKQVTVLGSPPVNVFLGVFAAPPLGSLFTNPQSPSPWN	89	
DB	23	TGQAEQPEVYVNTTNGSVRGYQVKNMAERSVNVFLGPFAPKPVGPFRFSRQPPERKKG	82	
QY	90	LREATSYPNLCLQNSEWILLDOHML-----KVHYPKFVSEDCULNIYAPAHADTGSKL	144	
DB	83	VRDAASYFPMCLQDK---VLGQYLSDAITNRKEKVRRLQISDCILNVYTPVSTBEQKL	139	
QY	145	PVLVWPFPGAFKTSASIFDGSALAYEDVLVVVQYRLGIFGFTTWDQAPGNMAFKD	204	
DB	140	PVFVWINGGGLVSGAASVDGSALAFDNNVVYTIQRLGAGYFSGDKKARNMGLD	199	
QY	205	QVALSWQKNIRFPFGDPSVTFEGRSAGIISVSLISPMAGLPHKAIMESGVAL-I	263	
DB	200	QVALQWIIQENTIHFRDPSGVTFEGRSAGVSVLVSPLAKGLHKALISBGTAVRI	259	
QY	264	PYLEAHVDEKSEDQVVAHFCGNNAUSDSEALLRLCLRTPKSKEL--LTLISQTKSPTRVVD	321	
DB	260	LFTF-----QBEQAGQRIIAAAGCKSSSALLVECLARKTEAMEQGITLKMPMPWTSASLD	315	
QY	322	GAFPNPBLDLSQAKFALPSITIGVNNHCGFLIP-MKEAPELSSNKSLSLAHLIONI	380	
DB	316	GVFPKSPROLISRKVINAVPYIIGVNNCEFGWLLPMMKFPETBELKEDVANQVLOST	375	
QY	381	LHI-----PQYLAHVNVEYFHDKHSLTBRDSLLDGLGVFVFPVLPALTARYARDGAP	435	
DB	376	LALFKAQPSDIYLVLVNBYIGVAENRAQVRDGLDIDAPLPLFVSVAEVARHHRDGNP	435	
QY	436	VYFYEFRHRPOCFEDTRPAFVKADHADEVRFVFGAFLKGDIVMFEQATEBEKLLSRKM	495	

RESULT 2  
 A34329  
 60K esterase (EC 3.1.1.-) Isoform 2 - rabbit  
 C:Species: *Oryctolagus cuniculus* (domestic rabbit)  
 C:Date: 22-Jun-1990 #sequence \_revision 22-Jun-1990 #text\_change 09-Jul-2004  
 R:Ozols, J.  
 U: Biol. Chem. 264, 12533-12545, 1989  
 A:Title: Isolation, properties, and the complete amino acid sequence of a second form of  
 A:Reference number: A34329, MUD:89308686, PMID:2745458  
 A:Accession: A34329  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-532 <OZO>  
 A:CrossReferences: UNIPROT:P14943  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase  
 F:32-517/Domain: cholinesterase homology <CHE>  
 F:201,430/Active site: Ser, His #status predicted

RESULT 3  
JC5408  
carboxylesterase (EC 3.1.1.1) - human  
C/Species: Homo sapiens (man)  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: JC5408  
R/Schwer, H.; Langmann, T.; Daig, R.; Becker, A.; Aslanidis, C.; Schmitz, G.  
Biochem. Biophys. Res. Commun. 233, 117-120, 1997  
A/Title: Molecular cloning and characterization of a novel putative carboxylesterase, pr  
A/Reference number: JC5408; MUID:97289502; PMID:9144407  
A/Accession: JC5408  
A/Molecule type: mRNA  
A/Residues: 1-559 <SCH>  
A/Cross-references: UNIPROT:O00748; GB:X09616; NID:g2058317; PIDD:CA470831.1; PID:g2058317  
A/Experimental source: intestine  
C/Comment: This enzyme hydrolyses many xenobiotics, such as carboxyl esters, thioesters &  
C/Genetics:  
A/Gene: GDB:CE82; JCR; CE2  
A/Cross-references: GDB:9959011  
C/Superfamily: cholinesterase; cholinesterase homology  
C/Keywords: carboxylic ester hydrolase; glycoprotein  
F:58-544/Domain: cholinesterase homology <CHE>  
F:115-95,123-280,291-428/Disulfide bonds: #status predicted  
F:111,276/Binding site: Ser, His (covalent) #status predicted  
F:228,457/Active site: Ser, His #status predicted

RESULT 4  
S47655  
carboxylesterase (EC 3.1.1.1) precursor - golden hamster  
C:Species: Mesocricetus auratus (golden hamster)  
C:Date: 26-Dec-1994 #sequence\_\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: S47655



```

Db      11 LAVCPIIGH-----SLRPVVDTTQGVKVLGKYSLSBGEQPVAVFLGVFPKAPPLGS 62
Qy      76 LRFTNPQAPSPMDNLRKATSYPNLCLONSEM---LLLDQHLKVNHPKFGVSDCLYNIY 133
Db      63 LRFAPOPAPSPMDNLRKATSYPNLCLONSEM---LLLDQHLKVNHPKFGVSDCLYNIY 133
Qy      134 APAAADUGSLPVLVWFPFGAFKFGSASIFDGSALAAVEDVLVWVVOYRLGIFGFTTWD 193
Db      123 SPADLTSSQLPVMVWVHGGGLVIGGRSPYNGALSAHENVVYIIRLGIWGLFSTGD 182
Qy      194 QHAPGNWAFKQVAAALSMVKNIIEFGGDPSSVTIFGSAGAISSVSLISPPAKGLFHK 253
Db      183 EHSPPGNWALDQALALRMVQDNIANFGGNPDSVTIFGSSSGGISVSIVLSPICKDLPFR 242
Qy      254 AIMSGLVAILPYLEAHDIYKESDLOVVAHPCGNNADEALRCIRKRPSEILLTSS---310
Db      243 AISESSGVVNTNWKKNIOAVNEIATLSQC---NDTSAAVVOCLRKOTSEILLTSSGKL 300
Qy      311 -QKTSFTRVNDGAFPPNBPDLISQKAFKAIISILGVNHEGCFLLPM---KEAPE-IL 365
Db      301 VOYNISLSTWIDGVVLPKAPBEILAEKSFNTVPYIVFKNQEGWIIIPMMLQVLLPEGM 360
Qy      366 SGNKSLALHLIQLNLIHPQYLLHVNEXFHDHGLTEIRDSILDLGLDGFVVPVALIT 425
Db      361 NBETASLILRRFHELSINSESMIPAVIEOYLKRGVDPKAKSELILMFGDIFFGIPAVLL 420
Qy      426 ARYHRDAGAPVYFEPFRRPQCFEDTKPAFVKAHDDEVRFVFGAFKGLKGIWEGATE 485
Db      421 SRSIRLDAGVSTYVYEFRRPSPVSDKRPQVTEBDHDEIFPFVFGAPLTK-----EGASE 474
Qy      486 EEKLSRRMMKYVATFARTGNPGNDLSLWPAVNLTEOYLQDLNMSLGGRLKBERVDFW 545
Db      475 EETLSQVKKKFWANFARNNGNPGEGLPMMPEYDEQEGYLGATTOAQRLKAEVAFW 534
Qy      546 TSTI 549
Db      535 TELL 538

```

## RESULT 7

```

S19307
C:Species: Rat
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C:Accession: S19307; MUID:92070571; PMID:1959668
R:Matsumura, M.; Inoue, H.; Ichinose, M.; Tanaka, S.; Miki, K.; Kurokawa, K.; Takahashi, T.
A:Title: The nucleotide and deduced amino acid sequences of porcine liver proline-beta-T
A:Reference number: S19307; MUID:92070571; PMID:1959668
A:Accession: S19307
A:Molecule type: mRNA
A:Residues: 1-566 <MAT1>
A:Cross-references: UNIPROT:Q29550; EMBL:X63323; NID:G1930; PIDN:CAA44929.1; P1D:G1931
A:Accession: S23607
A:Molecule type: protein
A:Residues: 19-40 <MAT2>
A>Note: 28-Lys and 33-Leu were also found
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; homotrimer
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-566/Product: carboxylesterase #status experimental <MAT>
F:51-552/Domain: cholinesterase homology <CHE>
F:80/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:222,467/Active site: Ser, His #status predicted

```

## Query Match

```

Best Local Similarity 37.8%; Score 1162.5; DB 2; Length 566;
Matches 250; Conservative 71; Mismatches 202; Indels 41; Gaps 8;
Qy      12 WCFPILOPLGHRQMGKTPSAGPQRTNRLGMIQKQVTVLGSPPVNVVFLGVFPKAP 71
Db      2 WLPPLVLSLSSATW--AGOPASPPVVDTAQGVILGKVSLEGLAQPVAIVFLGVFPKAP 59

```

```

Qy      72 PLGSIRFTNPQAPSPMDNLRKATSYPNLCLONSEM---SEMLLDQHLKVNHPKFGVS 124
Db      60 PLGSIRFAPOPAPSPMDNLRKATSYPNLCLONSEM---SEMLLDQHLKVNHPKFGVS 124
Qy      125 EDCIYLIYAAAHADTGSKLPLVWFPFGAFKFGSASIFDGSALAAVEDVLVWVVOYRLG 184
Db      115 EDCIYLIYTPADLTJRGRLPVWVHGGGLVIGGAPMIDGVVLAHENVVYIIRLGIWGL 174
Qy      185 IGFFTTWDQAHAGNNAFQVAAALSMVKNIIEFGGDPSSVTIFGSAGAISSVSLISPP 244
Db      175 IWGFSTGDSHSGNNGHLDQVAAALSMVKNIIEFGGDPSSVTIFGSAGAISSVSLISPP 244
Qy      245 PMAKGLFHKAIMESGVALIIPYLEAHDIYKESDLOVVAHPCGNNADEALRCIRKRPSE 304
Db      235 PLKAVLFRHAISSGVALIIPYLEAHDIYKESDLOVVAHPCGNNADEALRCIRKRPSE 304
Qy      305 ELLTTSQKTSFT-----RVNDGAFPPNBPDLISQKAFKAIISILGVNHEGCFLLPM 349
Db      293 ELLDITLTKKKFLLDPFHGDQSRHFPVVDGVVLPKAPBEILAEKSFNTVPYIVFKNQ 352
Qy      350 HEGGFLPKKAPKAPILSGS-NKSLALHLIQLNLIHPQYLLHVNEXFHDHGLTEIRDS 412
Db      353 QERGMFLPTMNGFPPLSEKLDOKTATSLMKSYPIANIPELIPVATDKLGSTDVPVK 412
Qy      406 KSLDLGLDGVFFVVPALITARYHRDAGAPVYFEPFRRPQCFEDTKPAFVKAHDDEVRF 465
Db      413 KDLFLDGLDGVFFVVPALITARYHRDAGAPVYFEPFRRPQCFEDTKPAFVKAHDDEVRF 465
Qy      466 FVFGAFKGLKGIWEGATEEELSKRMKYVATFARTGNPGNDLSLWPAVNLTEOYLQDLN 525
Db      473 SVFEPFLKGD-----APEEVSLSKTVKFWANFARNNGNPGEGLPMMPEYDEQEGY 526
Qy      526 QLDNMSLGGRLKBERVDFWSTI 549
Db      527 QIGVTOAKRLKGEVAFWINDL 550

```

## RESULT 8

```

UJ0054
C:Species: Rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Aug-1998
C:Accession: UJ0054
R:Takagi, Y.; Morohashi, K.; Kawabata, S.; Go, M.; Omura, T.
A:Title: Molecular cloning and nucleotide sequence of cDNA of microsomal carboxylesterase
A:Reference number: UJ0054; MUID:89174514; PMID:3235453
A:Accession: UJ0054
A:Molecule type: mRNA
A:Residues: 1-549 <YAK>
A:Experimental source: liver
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein; microsome
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-549/Product: carboxylesterase #status predicted <SIG>
F:50-538/Domain: cholinesterase homology #status predicted <MAT>
F:79,274,302,375,476/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:221,453/Active site: Ser, His #status predicted

```

## Query Match

```

Best Local Similarity 37.2%; Score 1144; DB 2; Length 549;
Matches 238; Conservative 92; Mismatches 183; Indels 34; Gaps 9;
Qy      16 LIIQPLGHRQMGKTPSAGPQRTNRLGMIQKQVTVLGSPPVNVVFLGVFPKAPPLGS 75
Db      11 LAVCPIIGH-----PSSP-PVVDITRGKVLGKVSLEGTQVAVFLGVFPKAPPLGS 62
Qy      76 LRFTNPQAPSPMDNLRKATSYPNLCLONSEM---SEMLLDQHLKVNHPKFGVSDCL 128
Db      63 LRFAPEPEPSPMDNLRKATSYPNLCLONSEM---SEMLLDQHLKVNHPKFGVSDCL 117
Qy      129 YNITAPAAADUGSLPVLVWFPFGAFKFGSASIFDGSALAAVEDVLVWVVOYRLGIFG 188

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QY 468 FGAFLKGDIVMEGATEEELSLRKMKYATPARTGNNGNDLSLMPAYNLTEQYLQ 527  
 Db 476 FGAFLK-----EGASEEIRLSKVMKFMANFARNGNNGEGLPHEVYNQEGYLOI 529  
 QY 528 DLMSIGORLKEPRVDFTS 547  
 Db 530 GANTQAOKLKEVAFTN 549

## RESULT 10

carboxylesterase (EC 3.1.1.1) ES-4 precursor, liver - rat  
 N/Alternate names: hydrolyase B  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
 C/Accession: S62788; S51203; A55304; S49257  
 R/Robbi: M. van Schaalingen, E. Beaufay, H.  
 Biochem. J. 313, 821-826, 1996  
 A/Title: Cloning and sequencing of rat liver carboxylesterase ES-4 (microsomal palmitoyl  
 A/Reference number: S62788; MUID:96190723; PMID:861161  
 A/Accession: S62788  
 A/Molecule type: mRNA  
 A/Residues: 1-561 <ROB>  
 A/Cross-references: UNIPROT:Q64573; EMBL:X81825; NID:9550417; PIND:CAAS7419.1; PID:95504  
 R/Morgan, E.W., Yan, B., Greenway, D., Petersen, D.R., Parkinson, A.  
 Arch. Biochem. Biophys. 315, 495-512, 1994  
 A/Title: Purification and characterization of two rat liver microsomal carboxylesterases  
 A/Reference number: S51202; MUID:95077430; PMID:7986098  
 A/Accession: S51203  
 A/Molecule type: protein  
 A/Residues: 19-48 <MOR>  
 A/Experimental source: liver  
 R,Yan, B., Yan, D., Brady, M., Parkinson, A.  
 J. Biol. Chem. 269, 29688-29696, 1994  
 A/Title: Rat kidney carboxylesterase. Cloning, sequencing, cellular localization, and re  
 A/Reference number: A55304; MUID:95050819; PMID:7961958  
 A/Accession: A55304  
 A/Molecule type: mRNA  
 A/Residues: 1-6, 'P', '61-212, 'A', 214-252, 'T', 254-309, 'IT', 312-341, 'N', 343-424, 'FY  
 A/Note: the sequence in Genbank entry RNU10697, release 107, (PID:9562008) has the codon  
 R/Robbi, M., Beaufay, H.  
 Submitted to the EMBL Data Library, September 1994  
 A/Reference number: S49257  
 A/Accession: S49257  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-561 <RO2>  
 A/Cross-references: EMBL:X81825; NID:9550417; PIND:CAAS7419.1; PID:9550418  
 C/Function:  
 A/Description: catalyzes conversion of carboxylic ester to alcohol and carboxylic anion  
 C/Superfamily: cholinesterase; cholinesterase homology  
 C/Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver  
 F.1.18/Domin: signal sequence #status predicted <SIG>  
 F.1.18/Product: carboxylesterase ES-4 #status experimental <MAT>  
 F.1.50-551/Domin: cholinesterase homology <CHE>  
 F.1.50-551/Product: cholinesterase homology <CHE>  
 F.1.221/Active site: Ser, His #status predicted  
 F.1.301/Binding site: carboxylate (Aan) (covalent) #status predicted

Query Match 37.0%; Score 1139; DB 2; Length 561;  
 Best Local Similarity 43.4%; Pred. No. 1.5e-81;  
 Matches 243; Conservative 82; Mismatches 195; Indels 40; Gaps 10;

QY 15 FLILPGLGHGKGTGSAEGPQNTLGMIOGKQVTVLGPVNVVFLGVPAPAPLIG 74  
 Db 5 FLILSLATCVVYG--NPSSP-PVVDITTKGKVLGKTVSLBSGVTSVAVFLGVFAPAPLIG 61  
 QY 75 SLRFTNPAPSPMDLREATISYPMCLQNSFW-----LLDQHLKTVHYKFGVSEDCY 129  
 Db 62 SLRFPAPQAPAEWSPVKNVITTYPPMCSQDAKAGQRMNDLLTNREKIH---LEFSDCY 118

QY 130 LNIYAPAHADTGSGLPVLVWPPGAFKTSASIFDSALAAVEDVLVWVVOYRLIGIFGP 189  
 Db 119 LNIYAPADFTKNSRLPVMVWVHGGGMVLGGASTYDGRVLSAYENVVVAIQRLIGKGF 178  
 QY 190 TTWDQAPGNWAFKQVVALSWYQKNIIEFGGSSVTFPGSAGAISVSLILSPMAKG 249  
 Db 179 STGDEHSRGWGHLDQVLAHLWQDNIANFGDPSVTFPGSAGAFSVVLSPLTKN 238  
 QY 250 LFKAIMESGVAILIPLYEANDYKESDLOVVAHFCGNNAADSALLRCITRPSKELLTL 309  
 Db 239 LFKAIMESGVVFLPGLTKDVNPA--AKQIDMVGCEFTTSAIIVHLCKRQTEBELLT 296  
 QY 310 SQTK-----SFRVVDGAFPNEDLILSQAFPAISITGVNNHECGF 354  
 Db 297 MKKNILIKLSQKDNKESHYFLSTVDNVLPKDKETLAEKNFTVPIYIGINKOEGW 356  
 QY 355 LCP--KKEAPILSGNSKSLAHLIQ--NLIHPQYALVANEYFHDKSLTEIRDSL 409  
 Db 357 LFTVMGFEVPADVE-LDKKMAITLLEKPAISYGPEDIIPIAIEKTKGSDSIKINDGI 415  
 QY 410 LLDLGDVFPVVALITARYHRDAGAPVYFEPFRPQCFEDTKAPYKADHAEVRFPG 469  
 Db 416 LAFIGVSPSIPSVVWSHDHDAQAPTYMZYQYFSPSPQREKVVGDHADDIVSVFG 475  
 QY 470 GAFKGDIVMEGATEEELSLRKMKYATPARTGNNGNDLSLMPAYNLTEQYLQ 529  
 Db 476 AFILK-----DGASEEIRIKLSKVMKFMANFARNGNPNRGLPHPQDQKEEYLIQ 529  
 QY 530 NMSLIGORLKEPRVDFTSTI 549  
 Db 530 TTQOSORLKEEVAFTQL 549

## RESULT 11

carboxylesterase (EC 3.1.1.1) egaeyn - mouse  
 N/Alternate names: beta-glucuronidase endoplasmic reticulum-targeting protein; esterase-;  
 C/Species: Mus musculus (house mouse)  
 C/Date: 10-Feb-1995 #sequence\_revision 10-Feb-1995 #text\_change 09-Jul-2004  
 C/Accession: A55281  
 R/Ovnic, M.; Swank, R.T.; Fletcher, C.; Zhen, L.; Novak, E.K.; Baumann, H.; Heintz, N.; C  
 Genomics 11, 956-967, 1991  
 A/Title: Characterization and functional expression of a cDNA encoding egaeyn (esterase-;  
 A/Reference number: A55281; MUID:92147141; PMID:1783403  
 A/Accession: A55281  
 A/Status: preliminary  
 A/Molecule type: mRNA; protein  
 A/Residues: 1-562 <OVN>  
 A/Cross-references: UNIPROT:Q64176; GB:S80191; NID:9244727; PIND:AA821335.1; PID:9244728  
 C/Superfamily: cholinesterase; cholinesterase homology  
 C/Keywords: carboxylic ester hydrolase; endoplasmic reticulum  
 F.1.51-552/Domin: cholinesterase homology <CHE>  
 F.1.51-552/Product: cholinesterase homology <CHE>  
 F.1.222/Active site: Ser, His #status predicted

Query Match 37.0%; Score 1138.5; DB 2; Length 562;  
 Best Local Similarity 44.4%; Pred. No. 1.6e-81;  
 Matches 240; Conservative 76; Mismatches 195; Indels 29; Gaps 6;

QY 31 GSAEGPQNTLGMIOGKQVTVLGPVNVVFLGVPAPAPLIGSLRFTNPAPSPMDL 90  
 Db 19 GHPSPFVVDITGVQKVLGKTVSLBSGVTSVAVFLGVFAPAPLIGSLRFPAPAEWSPV 78  
 QY 91 REATSYPMCLQNSFWLLDQHLKTVHYKFGV--SEDCYINIVAPAHADTGSGLPVLV 148  
 Db 79 KNATSYPMCGFQDPVGVQIYVNDLLTNREKIPLOFSEDCYINITTPADLTYSDBLPVWV 138  
 QY 149 WFPGAFKTSASIFDSALAAVEDVLVWVVOYRLIGIFFTWQAHAGWMAFKQVAA 208  
 Db 139 WIFGGGLVAGASTYGVLSHENVVVIQRLIGIFFTWQAHAGWMAFKQVAA 198  
 QY 209 LSWVQKNIIEFGGSSVTFPGSAGAISVSLILSPMAKGLFKHAIMESGVAILIPLYEA 268

RESULT 12

A31584

carboxylesterase (EC 3.1.1.1) Precursor - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 21-May-1990 #sequence\_revision 03-Aug-1992 #text\_change 09-Jul-2004

C:Accession: A31584

R:Jiang, R.M.; Satoh, H.; Martin, B.M.; Kimura, S.; Gonzalez, F.J.; Pohl, L.R.

Biochem. Biophys. Res. Commun. 156, 866-873, 1988

A:Title: Rat liver carboxylesterase: cDNA cloning, sequencing, and evidence for a multi-

A:Reference number: A31584; MUID:89050119; PMID:2973315

A:Accession: A31584

A: Molecule type: mRNA  
A: Residues: 1-540 <LON>  
A: Cross-references: UNIPROT: P10959; GB: M20629; GB: X13587; NID: g203279; P1DN: AAA40871.1;  
C: Superfamily: cholinesterase; cholinesterase homology  
C: Keywords: carboxylic ester hydrolase; glycoprotein  
F: 1-9/Domains: signal sequence #status predicted <SIG>  
F: 10-540/Product: carboxylesterase #status predicted <CAT>  
F: 41-529/Domains: cholinesterase homology <CHR>  
F: 70, 285, 286, 293, 366, 467/Binding site: carbonyl-ate (Aan) (covalent) #status predicted  
F: 212, 444/Active site: Ser, His #status predicted

Query Match	36.7%	Score 1129.5;	DB 2;	Length 561;
Best Local Similarity	43.4%	Pred. No. 8.3e-81;		
Matches 236, Conservative	83;	Mismatches 188;	Indels 37;	Gaps 9

```

QY 31 GPBAEGQOKRTKLGMLGKQVYLVGSSVFNANVGJVPFAAFPLSLKRTINQJPSFWJNL
Db 18 GNPSSPVVDVTMGKVKVLGKYASLEGVYQSVAVFLGVPFAKPLSLGFRAPQBPAPBWSFV
QY 91 REATSYNCLQNSW-----LLDDHMLKVHYKPFQVSEBCLYNTYAPAHADGSLP 145
Db 78 KNTTTPYPMCSQATKQGMNDLITNKEKH--LQSEBCLYNTYTPDDFTQDSMP 134
QY 146 VLVMPGAGKTKTSASIFDGSALAYEDVLVWVVOYRLGIFGFETTDQHPGNWAFKQ 205
Db 135 VMWVIRHGGLTQGSASTYDGRVLSAYENVVVALQYRLGINGFSTGDBHSGRMGHLD 194
QY 206 VVALSWYQKNIIEFFGDPSSYTFIGESAGALSVSSLSPAKGLFKHAIMESGVAITPY 265
Db 195 VVALHWQODNIANFGDPSGVTTFGESAGGSFVSVLVLSPLSKMLYHRAISEGVLLTQ 254
QY 266 LEAHDYKSENDLOVAFHFCGNMNASDSEALRLCLRTKPSKELLTYSOK-----TK 314
Db 255 LFTKDVAPRA--AQOIAMAGCKTTTSAIYHCLRQKTEBELLETMEKNKMLIKLSQRTK 312
QY 315 S-----FTRVVDGAFEPNEPLDLLSQAKFAPSIIGVNNHCGFLP--MKEADEILSGS 368
Db 313 ESYHFLSTVTDVVLPRDPKEILAEKQFNTPVPIVGINKOCGMLLPTMHRFVBPDVK-L 371
QY 369 NKCAIATLTQ--NTIHTBPQVLYLVANREYEHDKSITETIPDSLLDLIGQVFPVVALIT 425

```

```

Db      372 DKKATMLLEKFASTYICPEDIPVAIEKRGSDPPIKIRGCIATFGDVLFCIPSVTV
Qy      426 ARYRDAGAVFYEFYFHRPQCFEDTKPAFYADNADHDEVRVFGAFLKGIWMEGATE
Db      432 SRDRDAGAPTYEYEQYDPSFSSPQRKDVGDHADDVYVFCAPIIR-----DGASE
Qy      486 EELTLRKMKKYATATFARNGPNNDLSMPAYNLTEQYLQDLNMSLSGRLKEPRDVF
Db      486 EELTLRKMKKYATATFARNGPNNDLSMPAYNLTEQYLQDLNMSLSGRLKEPRDVF
Qy      546 TSTI 549
Db      546 TOLL 549

```

## RESULT 14

```

JC2447
C:Species: Rattus norvegicus (Norway rat)
C>Date: 29-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C/Accession: JC2447; S23462
R:Robbi, M.; Beaufay, H.
Biochem. Biophys. Res. Commun. 203, 1404-1411, 1994
A>Title: Cloning and sequencing of rat liver carboxylesterase ES-3 (EGASYN).
A/Reference number: JC2447; MUID:95032008; PMID:7945287
A/Accession: JC2447
A/Molecule type: mRNA
A/Residues: 1-561 <ROB>
A/Cross-references: UNIPROT:Q63108; GB:X81395; NID:9550146; PIDN:CAA57158.1; PID:9550147
A/Experimental source: liver
R:Medda, S.; Proia, R.L.
Eur. J. Biochem. 206, 801-806, 1992
A>Title: The carboxylesterase family exhibits C-terminal sequence diversity reflecting
A/Reference number: S23460; MUID:92299008; PMID:1606962
A/Accession: S23462
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 503-554, 'R', 556-561 <MED>
A/Cross-references: EMBL:X65295; NID:957557; PIDN:CAA46390.1; PID:957558
C/Keywords: carboxylic ester hydrolase; cholinesterase homology
F/1-18/Domain: signal sequence #status predicted <SIG>
F/19-561/Product: carboxylesterase ES-3 #status predicted <MAT>
F/50-551/Domain: cholinesterase homology <CHE>
F/79,107,489/Binding site: carbonylate (Asn) (covalent) #status predicted
F/221,466/Active site: Ser, His #status predicted

```

## Query Match

```

Best Local Similarity 36.5%; Score 1123; DB 2; Length 561;
Matches 245; Conservative 86; Mismatches 193; Indels 56; Gaps 11;

```

```

Qy      13 CFFLIQLPLGHRMGKTGPSAGCPORNTRLGIQKQYTVGSPVNVFLGVFPAP 72
Db      2 CLVYLILVFLAFTAG--GHPSSLPVVDLTQGVKGLKYSLSGFTQPAVAVFGVFPAP 59
Qy      73 LGSIRFNPAPSPMNLREAPSYPLCLQN-----SEVLLDDHMLKVNHPK 121
Db      60 LGSIRFNPAPSPMNLREAPSYPLCLQN-----SEVLLDDHMLKVNHPK 121
Qy      122 GVSDECLVNTIYAPAHADTGSKLPLVWMPFGAFTGSATFDSGALAAVEDLVVVQY 181
Db      113 --SEDCVLTNITPDLTRDLPLVWVHGGGLVLSGASTYDGLASTHENVVVVVQY 170
Qy      182 RLGIREFFTQQAHPGNWAFDOVALSWQNIIEFFGDPSSVTIFGSAAGISVSS 241
Db      171 RLGIREFFTQQAHPGNWAFDOVALSWQNIIEFFGDPSSVTIFGSAAGISVSS 241
Qy      242 ILSPAKGLFHKALWESSVAIIPYL-BAHDYKESDQVVAHCGNNAADSEALRLCLRT 300
Db      231 VLSPLAKGLFHKALWESSVAIIPYL-BAHDYKESDQVVAHCGNNAADSEALRLCLRT 300
Qy      301 KPSKELTLGSKTSTFT-----RVVDGAFPPNBPRLDLGQKAFKAIPISTI 345

```

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Db      288 KTEBELTTLTKNLIFSIDLHGDSRQSPVPVYLVQGVLPKPEETLAEKQNTVPTVY 347
Qy      346 GVNNECCFLTP-MKEAPELISGNSKSLAHLQN---ILHIPPQYLHVAIEYFDKHS 401
Db      348 GINQEFQWILPTMANTPSPDMLDPTATSTLTKSSFLTNLPEEALPVAVEKYLRTDD 407
Qy      402 LTELRLSLDLGLVFFVVPALITARVYHRDAGAPVYEFYFHRPQCFDTPAPFKAHA 461
Db      408 PDRKQDLLELDIVIFGVPSIVSRGHRDAGARTWMEFQVRPSFSKMKSTVGDHG 467
Qy      462 DEVARFVGAFLLKGDIVMEFGATEBEKLSRKMKYATATFARTGNPNNDLSMPAYNL 521
Db      468 DEIVSVGAPRLG-----GTSKERINLSRKMKYATATFARTGNPNNDLSMPAYNL 521
Qy      522 EGYLQIGATTQQAQKLKEKVAFMSE-----LWAKPLHA 556
Db      522 EGYLQIGATTQQAQKLKEKVAFMSE-----LWAKPLHA 556

```

## RESULT 15

```

S10367
C:Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C/Accession: S10367; S12468; S51202; S23460; S14361
R:Robbi, M.; Beaufay, H.; Octave, J.N.
Biochem. J. 269, 451-458, 1990
A>Title: Nucleotide sequence of cDNA coding for rat liver pi 6.1 esterase (ES-10), a car-
A/Reference number: S10367; MUID:90351366; PMID:2386485
A/Accession: S10367
A/Molecule type: mRNA
A/Residues: 1-565 <ROB1>
A/Cross-references: UNIPROT:Q9R135; EMBL:X51974
A/Note: 168-Gln, 247-Lys, 423-Met, and 506-Asn were also found
A/Status: the sequence from Fig. 4 is inconsistent with that from Fig. 5 in having 265-Lys,
submitted to the EMBL Data Library, February 1990
A/Reference number: S12468
A/Accession: S12468
A/Molecule type: protein
A/Residues: 1-264, 'R', 266-565 <ROB2>
A/Cross-references: EMBL:X51974; NID:956898; PIDN:CAA3236.1; PID:956899
R:Morgan, E.W.; Yan, B.; Greenway, D.; Petersen, D.R.; Parkinson, A.
Arch. Biochem. Biophys. 315, 495-512, 1994
A>Title: Purification and characterization of two rat liver microsomal carboxylesterases
A/Reference number: S51202; MUID:95077430; PMID:7986098
A/Accession: S51202
A/Molecule type: protein
A/Residues: 19-48 <ROK>
R:Medda, S.; Proia, R.L.
Eur. J. Biochem. 206, 801-806, 1992
A>Title: The carboxylesterase family exhibits C-terminal sequence diversity reflecting t
A/Reference number: S23460; MUID:92299008; PMID:1606962
A/Accession: S23460
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-185, 'Q', 187-422, 'W', 424-505, 'N', 507-565 <MED>
A/Cross-references: EMBL:X65296; NID:957553; PIDN:CAA46391.1; PID:957554
R:Gaustad, R.; Sletten, K.; Lovhaug, D.; Fonnun, P.
Biochem. J. 274, 693-697, 1991
A>Title: Purification and characterization of carboxylesterases from rat lung.
A/Reference number: S14361; MUID:91190080; PMID:2012599
A/Accession: S14361
A/Molecule type: protein
A/Residues: 19-26, 'P', 28-37 <GAU>
C/Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; homotrimer
F/1-15/Domain: signal sequence #status predicted <SIG>
F/19-561/Product: carboxylesterase #status predicted <MAT>
F/50-551/Domain: cholinesterase homology <CHE>
F/79,489/Binding site: carbonylate (Asn) (covalent) #status predicted

```

F:221,466/Active site: Ser, His #status predicted

Query Match 36.4%; Score 1121.5; DB 2; Length 565;  
Best Local Similarity 42.4%; Pred. No. 3,6e-80;  
Matches 245; Conservative 79; Mismatches 199; Indels 55; Gaps 11;

```
OY 12 WCFLLIOLPLGHRWGKTGPRAGPQNRTRIGIQKQVTVLGSPPVNNVFLGVFPAAP 71
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8 WLF-----LAACTAMGY--PSSP--PVNVTGKVLGKYVNLGCPAQPVAVFLGIPFAPK 58
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 72 PLGSIRFTNPQASPMWDLNREATSYPNLCLQN-----SEWLLDDQHMKNHYPKFGVS 124
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59 PLGSIRFAPQPAPAEPMNVKNTTSTYPMCSODAVGGQVLSLFTNRKENTIPLOF-----S 113
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 125 EDCLYNTIYAPAHADTGSKLPLYVWFPGCAFKTGSASIFDGSALAAEDVLVWVQYRLG 184
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 114 EDCLYNTIYTPADLTKNRSLRPVWVIHGGGLVVGASTYDGOVLSAHENVVVTIQRRLG 173
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 185 IFGFFTWDOHAPGNWAFKQVVALSWQNIIEFFGDPSSVTIFGESAGAISVSLLIS 244
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 174 IWFPGSTGDEHSRGWGHLDQVAAALHWQDNINANGNPGSVTIFGESAGGFSVSALVLS 233
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 245 PMAKGLFHKAIMESGVALIIPYLEADRYEKSEDLQVVAHFCGNASDSEALLRCLRTPEK 304
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 234 PLAKKLFHRAISESGVLTSLALITTDKRPINL--IATLSGCKTTSAVMVHCLRQKTED 291
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 305 ELTLTSOKTKSF-----TRVVDGAFPPNEPLDLSOKAFKAIPTSIIGVNN 349
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 292 ELLETSLKLNLFKLDLLGNPKESYPLPTVIDGVLPKTPETILAKSFNTVPIYIGINK 351
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 350 HECGFLFPMKEAPEILSG-----SNKSLALHLIONILHIPOYLHLVANEYFHDKSLTE 404
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 352 QEPGWIIPTLMGYPLSEKLDQKTKSL-LWKSYPCLKISEKMI PVVAEKYCGTDDPAK 410
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 405 IRDSLDDLGGVFPVVPALITARYHDAAGAPVYFEFRHRPOCFEDTKPAFYKADHADEV 464
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 411 RKDLFPQDLVADVIFGVPVWVSRSHRDAGAPTFYEFERPSFVSAMRPKTVIGDHGDEL 470
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 465 RFVFGGAFLLKGDIVWFEGATEEEKLSRMMKCYWATPARTGNPNGNDLSLMPAYNLTEOY 524
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 471 RSVFGSPFLK-----DQASEETVLSKVMKYMNFANRNGSPNGGGLPHMPEYDQKEGY 524
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 525 LQDLNMSIGORLKEPRVDFTWTSTIPLILSASDMLHSP 562
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 525 LKIGASTQAQRLKDKVAFWSE-----LRAKEAAEBP 557
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Search completed: June 16, 2005, 20:45:45  
Job time : 45 secs



## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 20:27:00 ; Search time 179 seconds  
(without alignments)  
1662.112 Million cell updates/sec

Title: US-10-674-636-2  
Perfect score: 3079  
Sequence: 1 MPQGLTSSASQWCFILQP.....PLSLTFLSLQPFPCAP 581

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2915	94.7	575	2	Q6NTJ32
2	2606	84.6	525	2	Q6DND9
3	2454	79.7	469	2	Q8N8C8
4	2250	73.1	575	2	Q6AW47
5	2094.5	68.0	575	2	Q6AW46
6	1985	64.5	545	2	Q81034
7	1676.5	54.4	361	2	Q95KH3
8	1298.5	42.2	557	1	SASB_ANAPL
9	1283.5	41.7	561	2	Q91W60
10	1281	41.6	559	2	Q8BK48
11	1276.5	41.5	559	2	Q35533
12	1271	41.3	559	2	Q8BM97
13	1266.5	41.1	556	2	Q6PD87
14	1263.5	41.0	568	2	Q6GMS4
15	1262.5	41.0	561	2	Q70177
16	1260.5	40.9	560	2	Q8R097
17	1257.5	40.8	554	2	Q35535
18	1239.5	40.3	562	2	Q6P306
19	1238	40.2	558	2	Q8K3R0
20	1237.5	40.0	558	2	Q8GZK3
21	1237.5	40.0	532	1	EST2_RABIT
22	1230	39.9	559	1	EST2_HUMAN
23	1213.5	39.4	561	2	Q70631
24	1213.5	39.4	566	2	Q766D7
25	1213.5	39.4	566	2	Q6E4S9
26	1210.5	39.3	557	2	Q640T6
27	1199	38.9	561	1	EST1_MESAU
28	1191	38.7	586	2	Q61PK9
29	1187.5	38.6	568	2	Q6PG74
30	1187.5	38.6	572	2	Q810S9
31	1186.5	38.5	554	1	ESTM_MOUSE

32	1183	38.4	565	2	Q95N05	Q95N05 canis famli
33	1179.5	38.3	571	2	Q6UW8	Q6UW8 homo sapien
34	1179	38.3	568	2	Q726J1	Q726J1 homo sapien
35	1175	38.2	565	2	Q8TD29	Q8TD29 homo sapien
36	1171.5	38.0	568	2	Q8VCU1	Q8VCU1 mus musculu
37	1169.5	38.0	561	2	Q91W60	Q91W60 mus musculu
38	1164	37.8	565	2	Q97582	Q97582 sus scrofa
39	1162.5	37.8	555	2	Q6GMJ1	Q6GMJ1 brachydanto
40	1162.5	37.8	566	1	EST1_PIG	Q29550 sus scrofa
41	1159.5	37.7	566	2	Q464Z1	Q464Z1 macaca fasc
42	1150.5	37.4	565	1	EST1_RABIT	P12337 oryctolagu
43	1150	37.3	564	2	ESTN_MOUSE	P23953 mus musculu
44	1149	37.3	565	2	Q35534	Q35534 mesocricetu
45	1144	37.2	549	1	EST1_RAT	P10959 rattus norv

ALIGNMENTS

RESULT 1  
Q6NTJ32 PRELIMINARY; PRT; 575 AA.  
AC Q6NTJ32.  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE FLJ31547 protein.  
GN Name=FLJ31547;  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
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Query Match 94.7%; Score 2915; DB 2; Length 575;  
 Best Local Similarity 97.0%; Pred. No. 6,2e-214;  
 Matches 553; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

12 WCFPILOPLGHRMGKTPSABEGPONTPLTIGKQVTVLGSPPVNVFLGVPAP 71  
 14 WAIWTLAAR-----TKGSAEPOKNNLIGIQGVTVLGSPPVNVFLGVPAP 65  
 72 PLGSRFTNPPASPMWDLREATSYPNLCLQNSEWMLLDHMLKVHPKFGVSEDCLYN 131  
 66 PLGSRFTNPPASPMWDLREATSYPNLCLQNSEWMLLDHMLKVHPKFGVSEDCLYN 125  
 132 IYAAHADTSGSKLPLVWVFGAGFKTGSASIPGCSALAAVEDLVVVVYRIGIFGFTT 191  
 126 IYAAHADTSGSKLPLVWVFGAGFKTGSASIPGCSALAAVEDLVVVVYRIGIFGFTT 185  
 192 WDOHAPGNMAFKQVVALSWQKNIEFGGDPSSVYTFGSGAGISVSSLISPMAGLIF 251  
 186 WDOHAPGNMAFKQVVALSWQKNIEFGGDPSSVYTFGSGAGISVSSLISPMAGLIF 245  
 252 HKAIMESGVALIIPLEAHDEKSEDIQVVAHFGNNAASDEALLRCLRTKPSKELLTISQ 311  
 246 HKAIMESGVALIIPLEAHDEKSEDIQVVAHFGNNAASDEALLRCLRTKPSKELLTISQ 305  
 312 KTSFTRVVVDGAFENEPIDLLSQKAFKAIPIIIGVNNHCEGFLPMKEAPEIISGSNKS 371  
 306 KTSFTRVVVDGAFENEPIDLLSQKAFKAIPIIIGVNNHCEGFLPMKEAPEIISGSNKS 365  
 372 LALHLQNTLHITPROVLIHVNANEPYDGLSLTEIDSLDLDIGVFFVVPALITARYARD 431  
 366 LALHLQNTLHITPROVLIHVNANEPYDGLSLTEIDSLDLDIGVFFVVPALITARYARD 425  
 432 AGAPVYFYEFRHRPOCFEDTKPAFYKADHAEVRFVPGAFKAGDIWFEATTEELLS 491  
 426 AGAPVYFYEFRHRPOCFEDTKPAFYKADHAEVRFVPGAFKAGDIWFEATTEELLS 485  
 492 RROMKYMATFARTGPNNDLSIMPAVYLTQYIQLDINLSGRLKEPVDWTSTIPL 551  
 486 RROMKYMATFARTGPNNDLSIMPAVYLTQYIQLDINLSGRLKEPVDWTSTIPL 545  
 552 ILSASDMHSPSLSLTFLSLQLPFFFCAP 581  
 546 ILSASDMHSPSLSLTFLSLQLPFFFCAP 575

## RESULT 2

OC6DN9 PRELIMINARY; PRT; 525 AA.  
 AC OC6DN9, 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
 DE Hypothetical protein FLJ31547.  
 GN Name=FLJ31547.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI TaxID=9606;  
 RN SEQUENCE FROM N.A.  
 RP PubMed=14702039; DOI=10.1038/ng1285;  
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
 RA Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahata K.,  
 RA Murakami K., Yasuda T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Sudo H., Hosori T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,  
 RA Abe K., Kamihira K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,  
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,  
 RA Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y., Ishida S.,  
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,  
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,

RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,  
 RA Musashino K., Yuki H., Oshima A., Sasaki N., Aotsuka S.,  
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,  
 RA Moriya S., Komiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
 RA Fujimori Y., Komiyama K., Taehiro H., Taniguchi S., Fujiyama T.,  
 RA Oono T., Yamada K., Fujii Y., Ozaki K., Hirota M., Omori Y.,  
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 RA Oktant R., Kawakami T., Noguchi S., Itoh T., Shigeta S., Senba T.,  
 RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
 RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu K., Senba T.,  
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R.,  
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,  
 RT "Complete sequencing and characterization of 21,243 full-length human  
 RT cDNAs.";  
 RL Nat. Genet. 36:40-45(2004).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PCR rescued clones;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strasserberg R.L., Feingold E.A., Grouse U.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stampleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uesdin T.B., Toshlyko S., Carninci P., Frange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz R., Krzywinski M.I., Skalka U., Smalms D.E., Scherch A.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PCR rescued clones;  
 RA Strasserberg R.L.;  
 RL Submitted (Apr.-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 DR EMBL; AK056109; BAB71094.1; -;  
 DR EMBL; BC069548; AAH69548.1; -;  
 DR HSSP; F12337; 1K4Y.  
 DR GO; GO:0016787; P:hydrolase activity; INA.  
 DR InterPro; IPR002018; Carboxylesterase.  
 DR Pfam; PF00135; Ser\_esterase.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Hydrolyase, Hypothetical protein.  
 SQ SEQUENCE 525 AA; 58200 MW; 77248788BA22F215 CRC64;

Query Match 84.6%; Score 2606; DB 2; Length 525;  
 Best Local Similarity 90.9%; Pred. No. 2,2e-190;  
 Matches 501; Conservative 0; Mismatches 0; Indels 50; Gaps 1;  
 31 GPSAEGPQRNTRLGWIGKQVTVLGSPPVNVFLGVPAPPLGSRFTNPPASPMWDL 90  
 25 GPSAEGPQRNTRLGWIGKQVTVLGSPPVNVFLGVPAPPLGSRFTNPPASPMWDL 84  
 91 REATSYNPLCLQNSEWMLLDHMLKVHPKFGVSEDCLYNIAAHADTSGSKLPLVWV 150  
 85 REATSYNPLCLQNSEWMLLDHMLKVHPKFGVSEDCLYNIAAHADTSGSKLPLVWV 144

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OY 151 PGAFKTSASIFDGSALAAVEDVLVVVVOYRLGIFGFTTMDQHPAGNMAFKQVAAIS 210
DB 145 PGAFKTSASIFDGSALAAVEDVLVVVVOYRLGIFGFTTMDQHPAGNMAFKQVAAIS 204
OY 211 WVKRIEFGDPSVITFGESAGASISVLSLMSMAGLTHKAIMESGVALIIPYLEAND 270
DB 205 WVKRIEFGDPSVITFGESAGASISVLSLMSMAGLTHKAIMESGVALIIPYLEAND 264
OY 271 YKESBDLVVVAHFCNNASDSEBALRCRTKPSKELLTQSOKTSFTVVDGAFPPNEPL 330
DB 265 YKESBDLVVVAHFCNNASDSEBALRCRTKPSKELLTQSOKTSFTVVDGAFPPNEPL 324
OY 331 DLSQAKFAIPSIIGVNNHEGFLPMKEAPEILSGNSKSLALHILNLIHPQYALH 390
DB 325 DLSQAKFAIPSIIGVNNHEGFLPMKEAPEILSGNSKSLALHILNLIHPQYALH 384
OY 391 VANEFYHDKSLTEIRDSLLDLGDFVFPVLPALITARYHRDAGAVYVEFRHRPQCED 450
DB 385 VANEFYHDKSLTEIRDSLLDLGDFVFPVLPALITARYHRDAGAVYVEFRHRPQCED 424
OY 451 TKPAPVADHDEVRVFGAFLKGDIVMPEGATEEKLRSKMKYATFARTGNPKN 510
DB 425 -----BCATEEKLRSKMKYATFARTGNPKN 454
OY 511 DLSMPAYNLTEOYLQDLNMSLQRLKEPRVDFWTSTPILSASDMLHSPLSSTPLS 570
DB 455 DLSMPAYNLTEOYLQDLNMSLQRLKEPRVDFWTSTPILSASDMLHSPLSSTPLS 514
OY 571 LLQPEFFFCAP 581
DB 515 LLQPEFFFCAP 525

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## RESULT 3

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OY Q8NBC8 PRELIMINARY: PRT; 469 AA.
AC Q8NBC8;
DB 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein FLJ33678.
OS Homo sapiens (Human).
OC Eukaryota; Euteeria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohtsuka M., Nishitani T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hirakawa K., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanohori K., Takahashi-Fuji A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa T., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Teraishi Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Omori Y., Okamoto S.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

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RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Maehara Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45(2004).
CC -I- SIMILARITY: Belongs to the type-B carboxylesterase/1lipase family.
DR EMBL; AK090997; BAC03565.1; -.
DR HSP; P12337; 1K4Y.
DR CO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR002018; Carboxylesterase.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KM Hydrolyase.
SQ SEQUENCE 469 AA; 52312 MW; 7A186F66C10A9080 CRC64;

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Query Match 79.7%; Score 2454; DB 2; Length 469;
Best Local Similarity 99.6%; Pred. No. 7.8e-179;
Matches 467; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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OY 113 MLKHYPRGVSECLYINIAPAHADTGSRLPLVWFPFGAFKTSASIFDGSALAAVE 172
DB 1 MLKHYPRGVSECLYINIAPAHADTGSRLPLVWFPFGAFKTSASIFDGSALAAVE 60
OY 173 DVLVVVOYRLGIFGFTTMDQHPAGNMAFKQVAAISWVKRIEFGDPSVITFGES 232
DB 61 DVLVVVOYRLGIFGFTTMDQHPAGNMAFKQVAAISWVKRIEFGDPSVITFGES 120
OY 233 AGAISVSLSPNAKGLFHKAIMESGVALIIPYLEANDYEKSEBDLVVVAHFCNNASDSE 292
DB 121 AGAISVSLSPNAKGLFHKAIMESGVALIIPYLEANDYEKSEBDLVVVAHFCNNASDSE 180
OY 293 ALPCLRTKPSKELLTQSOKTSFTVVDGAFPPNEPLDLSQAKFAIPSIIGVNNHEC 352
DB 181 ALPCLRTKPSKELLTQSOKTSFTVVDGAFPPNEPLDLSQAKFAIPSIIGVNNHEC 240
OY 353 GFLPMKEAPEILSGNSKSLALHILNLIHPQYALHVVANEFYHDKSLTEIRDSLLD 412
DB 241 GFLPMKEAPEILSGNSKSLALHILNLIHPQYALHVVANEFYHDKSLTEIRDSLLD 300
OY 413 LGDFVFPVLPALITARYHRDAGAPVYVEFRHRPQCFEDTKAPYKADHDEVRVFGAF 472
DB 301 LGDFVFPVLPALITARYHRDAGAPVYVEFRHRPQCFEDTKAPYKADHDEVRVFGAF 360
OY 473 LKGDIVMEGATEEKLRSKMKYATFARTGNPNDLSMPAYNLTEOYLQDLNMS 532
DB 361 LKGDIVMEGATEEKLRSKMKYATFARTGNPNDLSMPAYNLTEOYLQDLNMS 420
OY 533 LGQALKERVDVFWTSTPILSASDMLHSPLSSTPLSLLQPEFFFCAP 581
DB 421 LGQALKERVDVFWTSTPILSASDMLHSPLSSTPLSLLQPEFFFCAP 469

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## RESULT 4

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OY Q6AM47 PRELIMINARY: PRT; 575 AA.
AC Q6AM47;
DB 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Carboxylesterase-like urinary excreted protein.
OS Name=cuxin;
OC Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteeria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=urine;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohtsuka M., Nishitani T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hirakawa K., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanohori K., Takahashi-Fuji A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa T., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Teraishi Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Omori Y., Okamoto S.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

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Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 DR EMBL: AB186392; BAD35015.1; -.  
 DR GO: GO:0003824; F:catalytic activity; IEA.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 DR Hydrolase.  
 KW SEQUENCE 575 AA; 63620 MW; 1005C35B82B183D CRC64;

Query Match 73.1%; Score 2250; DB 2; Length 575;  
 Best Local Similarity 75.7%; Pred. No. 4e-163;  
 Matches 417; Conservative 61; Mismatches 73; Indels 0; Gaps 0;

QY 31 GPSAEGQQRNTRLGKQKQVTVLGSPPVNVFLGVFPAPAPPGSRFTNPPQASPMNDL 90  
 DB 25 GPADADAPRSTRIGLVGWKQATVLGSTMVNLGIFPAAPFLGPRFKRPKPPALLMDS 84  
 QY 91 REATSYPNLCLQNSEMLLDQHLKHYPKFGVSEDCLYLNTYAPAHADTGSKLPLVMF 150  
 DB 85 RDAITSYKCLQNSWMLSDQHLKHYPNLVESEDCLYLNTYAPAHANTGSKLPVMWF 144  
 QY 151 PGGAFTGSAIFDGSALAAVEDVLVVVQYRLGIFGFTTWDQAPGMAFKQVALS 210  
 DB 145 PGGAFTGSAIFDGSALAAVEDVLVTVQYRLGIFGFTTWDQAPGMAFLDQALALT 204  
 QY 211 WYQKNIFFPGDPSVTITGESAGAISVSSLISPMAGLPHKAIMESGVAIIPYLEAND 270  
 DB 205 WYQENIEFGCDPHSTITGESAGAISVGLVLSPMASGLPHKAIMESGVAIIPFLNAPD 264  
 QY 271 YESGELOVVAHFCGNNADEALRLCTRKPSKELTLISOKTSFPRVNDGAFPRNEPL 330  
 DB 265 DERNEDELQYIARIICGNVSDVALLOCLRAKSSELDLANKTISFRVNDGFEFFDEPL 324  
 QY 331 DLSOKAFAPISIIIGNVNHGCFLLPMKEAPEILSGSNKSLALHLIQLNTLHPPQYLAH 390  
 DB 325 DLTETKTRPSISVIGNNHGCFLLPMKEPEPEILSGSNKSLALHLIHRVLIHPQYLYI 384  
 QY 391 VANEFYHDKSLTEIRDSLDLGDVFVVPALITARYHNDAGAPVYFEEFRPOCFED 450  
 DB 385 VADQYFNKHSPIVEIRDSFLDLGDVFVVPALITARYHNDAGAPVYFEEFRPOCFED 444  
 QY 451 TKPAFVKADHDEVRFVPGGAFLLKGDIVMEGATEEKKLSRQMKWATFARTGNPQN 510  
 DB 445 TRPAFVKADHDEVRFVPGGAFLLKGNIVMEGATEEKKLSRQMKWATFARTGNPQN 504  
 QY 511 DLSIPAVNLTEQYLQDLNMSLQRLKEPRVDFTMTSTIPLISASDMLHSPSLSTPLS 570  
 DB 505 GLPIMPAYSQSEQYLRKLDLNIISVQKLRQEVVEFMSDTPLIMSKSTADPGPPVLLSIS 564  
 QY 571 LLOPFFFCAP 581  
 DB 565 VLDPFLSSAP 575

RESULT 5

Q6AM46 PRELIMINARY; PRT; 575 AA.

ID Q6AM46  
 AC Q6AM46;  
 DT 25-OCT-2004 (Tremblrel. 28, Created)  
 DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
 DE Carboxylesterase-like urinary excreted protein.  
 GN Name=Cauxin;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Miyazaki M., Yamashita T., Taira H., Suzuki A.;

"cauxin family protein."  
 RT Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 DR EMBL: AB186393; BAD35016.1; -.  
 DR GO: GO:0003824; F:catalytic activity; IEA.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 DR Hydrolase.  
 KW SEQUENCE 575 AA; 64166 MW; 3EB9D85981D9D0A CRC64;

Query Match 68.0%; Score 2094.5; DB 2; Length 575;  
 Best Local Similarity 68.5%; Pred. No. 3e-151;  
 Matches 390; Conservative 69; Mismatches 99; Indels 11; Gaps 1;

QY 12 WCFEFLQPLUHRQMGKTPSAEGPQRNTRLGKQKQVTVLGSPPVNVFLGVFPAP 71  
 DB 17 WIFGALIE-----GSVTEEPHRYTKLGVWQKQATVRLRPVNVFLGIFPAAP 65  
 QY 72 PLGSLRFTNPQASPMNDLREATSYPNLCLQNSEMLLDQHLKHYPKFGVSEDCLYLN 131  
 DB 66 PLGSLRFTSKQPPRIMNDLREATYAPNLCFQNLNMLFTYQNLKVSYPILGMSDCLYLN 125  
 QY 132 IYAPAHADTGSKLPLVMFPGGAFTGSAIFDGSALAAVEDVLVVVQYRLGIFGFTT 191  
 DB 126 IYAPAHADTGSKLPLVMVPIPGGAFETGSAIFDGSALAAVEDVLVTVQYRLGIFGFTT 185  
 QY 192 WDQAPGMAFKQVALSWYQKNIFFPGDPSVTITGESAGAISVSSLISPMAGLPHK 251  
 DB 186 QNHAPGNWATPDALALWRENIKIFGAGNPSTVITFGNSAGAISISSILISPLSADLF 245  
 QY 252 HKAIMESGVAIIPYLEANDYKESDELQVVAHFCGNNADEALRLCTRKPSKELTLISQ 311  
 DB 246 HKAIMESGVAIIPLEKSDNDLKHDLQVVAHFCGNVSDKALKLKRKSSLELMSLSQ 305  
 QY 312 KTKSFTVVDGAFPPNPDLDSOKAFAPISIIIGNVNHGCFLLPMKEAPEILSGSNK 371  
 DB 306 KAKSFTVVDGAFPPNPDLDSOKKTLKIVPSTIGNNCECYIIPVDTPEILSGSNES 365  
 QY 372 LALHLINLHIPPQYLAHVAHYFPHDKSLTEIRDSLDLGDVFVVPALITARYHND 431  
 DB 366 TALTLHTLHPTQHLVYVKEVEFHGKSPDIDTLLDGDVFVVPALITARYHND 425  
 QY 432 AGAPVYFEERHPPQCFEDTKPAFYKADHDEVRFVPGGAFLLKGDIVMEGATEEKKLS 491  
 DB 426 SGAPVYFEERHPPQCFEDTKPAFYKADHDEVRFVPGGAFLLKGDIVMEGATEEKKLS 485  
 QY 492 RQMKWATFARTGNPQNDLSIPAVNLTEQYLQDLNMSLQRLKEPRVDFTMTSTIPL 551  
 DB 486 RQMKWATFARTGNPQNDLPPMPVYDENQYELDNISTGRRLDQVVEFTDTPL 545  
 QY 552 ILSASDMLHSPSLSTPLSLLOPFFFCAP 580  
 DB 546 ILSASDMLHSPSLSTPLSLLOPFFFCAP 574

RESULT 6

Q81034 PRELIMINARY; PRT; 545 AA.

ID Q81034  
 AC Q81034;  
 DT 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DE Carboxylesterase-like urinary excreted protein.  
 GN Name=Cauxin;  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Kidney; PubMed=12401131; DOI=10.1042/BJ20021446;  
 RX MEDLINE=22458314; Soera S., Taira H., Yamashita T.;  
 RA Miyazaki M., Kamie K., Soera S., Taira H., Yamashita T.;  
 RT "Molecular cloning and characterization of a novel carboxylesterase-  
 like protein that is physiologically present at high concentrations in  
 the urine of domestic cats (Felis catus).";  
 RL Biochem. J. 370:101-110(2003).  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 DR EMBL: AB045377; BAC22577.1; -.  
 DR HSSP: P12337; 1K4Y.  
 DR GO: GO:0016787; P:hydrolyase activity; IEA.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000379; Ser. ester.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KM Hydrolyase.  
 SQ SEQUENCE 545 AA; 60505 MW; 9F73FA693D271FA9 CRC64;

Query Match 64.5%; Score 1985; DB 2; Length 545;  
 Best Local Similarity 71.7%; Pred. No. 6,5e-143;  
 Matches 373; Conservative 60; Mismatches 85; Indels 2; Gaps 2;

QY 31 GSAAGPQNRRLGVIQGVQVTVLGVVNVVFLGVFPAPPLGSLRFTNPPAPSPWNL 90  
 DB 25 GBAADAPVSTRLGWVGKQTTLVSGTVVNMFLGIPYAAPPLGLRFPKQPPALFGNDF 84  
 QY 91 RQATSYVNLCLDNSEFLLDQHLKRVKPGVSEDCVLYNIYAPHAADTSGKLPLYWF 150  
 DB 85 RNATSYVPLKCFQDLLEVLVSQVHLKRVKPLBASEDCVLYNIYAPHAADTSGKLPLYWF 144  
 QY 151 PGCAFPTGSASIFDGSALAAEDVLVWVQVRLGIFGFTTDOHAPGNMAFKDQVAALS 210  
 DB 145 PGCAFPTGSASIFDGSALAAEDVLVWVQVRLGIFGFTTDOHAPGNMAFKDQVAALS 204  
 QY 211 WQKNIIEFGGDPSSVTTFGESAGATSVSLISPMAGLFFKAIWESGVAIIPYL-EAH 269  
 DB 205 WVRDNIIEFGGDPSSVTTFGESAGATSVSLISPMAGLFFKAIWESGVAIIPYL-EAH 264  
 QY 270 DYKESDLOVNAHFCGNMNSDEBALLRCRTKPSKELLTLOKTSFTTVQDAGPNNRP 329  
 DB 265 GDERKDDLOVNAHFCGNMNSDEBALLRCRTKPSKELLTLOKTSFTTVQDAGPNNRP 324  
 QY 330 LRLSOKAFKAPSIIGVNNHEGFLPMKEAPELISGNSKSLALHLIONIHIPQYLH 389  
 DB 325 VALLTOKANSPSTIGVNNHEGFLPMKEAPELISGNSKSLALHLIONIHIPQYLH 383  
 QY 390 LVANEFYHDKSLTEIRDSLLDLGDFVFPVLPALITARYHRDAGAPVYFEFRHRPQCFE 449  
 DB 384 LVADHFFYHDKSLTEIRDSLLDLGDFVFPVLPALITARYHRDAGAPVYFEFRHRPQCFE 443  
 QY 450 DTKPAFVKADHADVRFVFGAFLKGDIVMFGATSEEEKLSRKMKYATARTGNPNP 509  
 DB 444 DTKPAFVKADHADVRFVFGAFLKGDIVMFGATSEEEKLSRKMKYATARTGNPNP 503  
 QY 510 NDLSLMPAYNLTEBOYLQDLNMSLGORLKEPRVDFEFTSTI 549  
 DB 504 EGVPMLPATYOSBOYLQDLNMSLGORLKEPRVDFEFTSTI 543

RESULT 7  
 Q95KH3 PRELIMINARY; PRT; 361 AA.  
 AC Q95KH3;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OC NCB1\_Taxid=9541;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Temporal lobe right;  
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
 RA Suzuki Y., Sugano S., Hashimoto K.;  
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 DR EMBL: AB060873; BAB46884.1; -.  
 DR HSSP: P12337; 1K4Y.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR Pfam: PF00135; Coesterase; 1.  
 KM Hypothetical protein.  
 SQ SEQUENCE 361 AA; 41032 MW; AC62AB6E78C5F1A1 CRC64;

Query Match 54.4%; Score 1676.5; DB 2; Length 361;  
 Best Local Similarity 95.0%; Pred. No. 1.4e-119;  
 Matches 323; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

QY 242 ILSPMAKGLFFKAIWESGVAIIPYLKADYKESDLOVNAHFCGNMNSDEBALLRCCLRTK 301  
 DB 17 ILSPMAKGLFFKAIWESGVAIIPYLKADYKESDLOVNAHFCGNMNSDEBALLRCCLRTK 76  
 QY 302 PSKELLTLOKTSFTTVQDAGPNNRPDLISOKAFKAPSIIGVNNHEGFLPMKEA 361  
 DB 77 PSKELLTLOKTSFTTVQDAGPNNRPDLISOKAFKAPSIIGVNNHEGFLPMKEA 135  
 QY 362 PEILSGNSKSLALHLIONIHIPQYLHVNEXYHDKSLTEIRDSLLDLGDFVFPV 421  
 DB 136 PEILSGNSKSLALHLIONIHIPQYLHVNEXYHDKSLTEIRDSLLDLGDFVFPV 195  
 QY 422 ALITARYHRDAGAPVYFEFRHRPQCFEDTYPAPYKADHADVRFVFGAFLKGDIVNPE 481  
 DB 196 ALITARYHRDAGAPVYFEFRHRPQCFEDTYPAPYKADHADVRFVFGAFLKGDIVNPE 255  
 QY 442 GATEEEKLSRKMKYATARTGNPNNDLSMPAYNLTEBOYLQDLNMSLGORLKEPR 541  
 DB 256 GATEEEKLSRKMKYATARTGNPNNDLSMPAYNLTEBOYLQDLNMSLGORLKEPR 315  
 QY 542 VDFWSTIPLILSADMLSPSLTFLSLQPPFFCAP 581  
 DB 316 VDFWSTIPLILSADMLSPSLTFLSLQPPFFCAP 355

RESULT 8  
 SASB\_ANAPL STANDARD; PRT; 557 AA.  
 ID SASB\_ANAPL  
 AC 004791;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Fatty acyl-CoA hydrolyase precursor, medium chain (EC 3.1.2.-)  
 DB (Thioesterase B).  
 OS Anas platyrhynchos (Domestic duck).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.  
 OC NCB1\_Taxid=8839;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 26-65.  
 RC TISSUE=urogenital gland;  
 RX MEDLINE=93100823; PubMed=8314791;  
 RA Hwang C.-S., Kolatukudy P.E.;  
 RT "Molecular cloning and sequencing of the thioesterase B cDNA and  
 stimulation of expression of the thioesterase B gene associated with  
 hormonal induction of peroxisome proliferation.";  
 RT  
 RL J. Biol. Chem. 268:14278-14284(1993).  
 CC -1- FUNCTION: Fatty acid biosynthesis chain termination and release of  
 the free fatty acid product is achieved by hydrolysis of the thio  
 ester by a thioesterase. This thioesterase may play a role in the production of  
 CC peroxisome proliferation and may play a role in the production of  
 CC 3-hydroxy fatty acid diester phenones.  
 CC -1- TISSUE SPECIFICITY: Highest levels in urogenital gland, much lower  
 CC in liver and kidney.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC entities requires a license agreement (see <http://www.ebi.ac.uk/announcements>  
 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

DR EMBL: L05493; AAA49223.1; -  
 DR PIR: A47162; A47162.  
 DR HSSP: O7540; LK4Y.  
 DR InterPro: IPR002018; CarboxylesteraseB.  
 DR InterPro: IPR00379; Ser. ester.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 DR Direct protein sequencing; Fatty acid biosynthesis; Hydrolase; Signal.  
 FT SIGNAL 1 25  
 FT CHAIN 26 557 Fatty acyl-CoA hydrolase.  
 FT ACT\_SITE 227 227 Acyl-ester intermediate (By similarity).  
 FT ACT\_SITE 345 345 Charge relay system (By similarity).  
 FT ACT\_SITE 460 460 Charge relay system (By similarity).  
 FT DISULFID 93 122 By similarity.  
 FT CARBOHYD 476 476 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 557 AA; 61637 MW; 03E35D90A037FEB0 CRC64; (Potential).

Query Match 42.2%; Score 1298.5; DB 1; Length 557;  
 Best Local Similarity 48.4%; Pred. No. 1.9e-90;  
 Matches 265; Conservative 79; Mismatches 177; Indels 27; Gaps 8;

QY 30 TGPSAGPQNRPLGNIQKQVTVLGSVPVNVFLGVPPAAPPILSLFTNPQASPPMDN 89  
 DB 23 TGSKAQPEVTVYNGSVRGVQKVNAASRVVFLGLPFAKPVPPLRFSPPPEPWKG 82  
 QY 90 LREATSYNPLCLQNSEMLLDQHML-----KHVYKFEVSEDCLYLYAPAHADTSGKL 144  
 DB 83 VRDASVYPMCLQDK---VLGGYLSDAITTRKEXYRLQISDCLYLVNVTPESTEQEL 139  
 QY 145 PVLWVFPFGAFTKTSASIFDGSALAYEDVLVVVQVYLFIFGFTTMDHAGNNAFKD 204  
 DB 140 PFLVNIHGGGLVSGAASYSASALAFNIVVVTIQLRLGAGVFGTGDHAGNNGYLD 199  
 QY 205 QVALSWYQKNIIEFGDPSVITFGESAGLISVSLISPMAGLFFHKAIMSGVAL-1 263  
 DB 200 QVALQWVQENIIFRGDPSVITFGESAGVSVSALVLPKAGLFFHKAISSEGTAVRI 259  
 QY 264 PYLEAHYKESDIQVVAHFCGNASDSEALLRLCFLTKPSKEL--LTLSQTKTSFTRVVD 321  
 DB 260 LFTL-----QPEEQARIAAAAGCEKSSSALLVCLAKETAEHQITLTKMPMFISASID 315  
 QY 322 GAFPNPEPLDLLSQAKFAKPSIIIVNNHCGFLP-MKEAPEILSGSKSLALHLIQNI 380  
 DB 316 GVFFPKSPRLLSKVNAVPIYIIVNNCFEGMILPRMKPFPEFTGLEKQVAVQLQST 375  
 QY 381 LHT-----PQVYHLVANEYFHDKSLTEIRDSLLDLGDVFVVPALITAYHDAAP 435  
 DB 376 LAISFKGAPSDIVLVYNEYIIVANRAQVROGLDLSIDPLFVPSAAVEVAHHHDAQNP 435  
 QY 436 VYFYEFHHRQCEEDTKPAFVADADADVRFVFGAFLKGDITMEGATEEKLISRRKM 495  
 DB 436 VYFYEFQHPSSAAGVVFVADADADADVRFVFGAFLKGDITMEGATEEKLISRRKM 489  
 QY 496 KTWATFARTGNPNDLSLMPAVNLTEOYLQDLMLMSLQGLKPKRPVFTSTPLILSA 555  
 DB 490 KWTNVAARNGNPGEGLVHMPOYDMDERLEIDLTQKAKKLKGRKMEFWMLTEQIMSD 549  
 QY 556 SMLMSPL 563  
 DB 556 RRRKHTDL 557

Q91WGO ID Q91WGO PRELIMINARY; PRT; 561 AA.  
 AC Q91WGO  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
 DE Carboxylesterase 2 (Carboxylesterase M13 precursor).  
 CN Name=Ces2; Synonyms=ces2a3;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon, and Kidney;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshitsuki S., Carrinci F., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek A.M., Gay L.J., Hulik S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Whiting J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,  
 RA Krzywinski M.I., Skalske U., Smallus D.B., Schmech A., Schrein J.E.,  
 RA Jones S.J., Maira M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences".  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Kidney;  
 RX Strausberg R.;  
 RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RN [13]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RX Strausberg R.;  
 RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [14]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RX Strausberg R.;  
 RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [15]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon, and Kidney;  
 RX Strausberg R.;  
 RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 RP [16]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Liver;  
 RX MEDLINE=22744052; PubMed=12859986; DOI=10.1016/S0003-9661(03)00286-8;  
 RA Furuhata T., Hosokawa M., Nakata F., Satoh T., Chiba K.;  
 RT "Purification, molecular cloning, and functional expression of  
 RT inducible mouse liver acylcarnitine hydrolyase in C57BL/6 mouse,  
 RT belonging to the carboxylesterase multigene family".  
 RL Arch. Biochem. Biophys. 416:101-109(2003).  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 DR EMBL: BC015290; AAH15290.1; -  
 DR EMBL: BC024552; AAH24552.1; -  
 DR EMBL: BC031170; AAH31170.1; -  
 DR EMBL: BC034178; AAH34178.1; -  
 DR EMBL: BC034180; AAH34180.1; -  
 DR EMBL: BC034191; AAH34191.1; -  
 DR EMBL: AB110073; BAC76623.1; -

RESULT 9



DR HSPF, P1237, 1K4Y.  
 DR MGD, MGI:2385905; Cae2.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR Pfam; PF00135; Coesterase; 1.  
 DR PROSITE; PS00122; CARBOXYLESTERASE B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 DR KMW Hydrolyase; Signal.  
 FT SIGNAL 1 26 Potential.  
 FT CHAIN 27 561 carboxylesterase MJ3.  
 SQ SEQUENCE 561 AA; 62469 MW; F793967A64EB728 CRC64;  
 Query Match 41.7%; Score 1282.5; DB 2; Length 561;  
 Best Local Similarity 48.4%; Fred. No. 3.2e-89;  
 Matches 276; Conservative 77; Mismatches 174; Indels 43; Gaps 14;

14 FLLIOPLLGHOMGTGSPAGSPORNTLGMIOGQOVVLSPVNVVFLGVPAPPL 73  
 15 FELL--LIIHVQ--GODSPBA-NPIRNTTGTQIQQSLHVKTAKGVHTFLGIPPAKPV 70  
 74 GSLRFTNPQAPSPWNLREATSYPNLCIONSEML---LLDQMLKVHPKGVSEDCLY 129  
 71 GLRFRAPRPPAPSPWNVDRGTAPMPCIQNLMNLNAGLPDKMKMLSSFP---MSDCLY 127  
 130 LNIYAPAHADTSSKLPVLPVFGAGFKTSASIFDGSALAAVEDLVVVVYRLGIFGRF 189  
 128 LNIYTPAHMEGSNLPVWVWVHGALVIGMAGMFDGSLITVNEEDLVVVTIYVRLGVLPF 187  
 190 TTMDDHAPNMAFKQOVVALSWQKNIIEFGGDPSPVTIFGSSAGAISSVSLILSPMAG 249  
 188 STGDHARKNMGYLDQAAALRWQNIHAFGSPDRVTIFGSSAGTSSVSHVSPMSG 247  
 250 LFHKAIMESGVAIIPLEAHNDEKSEDLQ--VVAHFQGNASDEALLRCLRTKPSKELT 308  
 248 LFHGAIMESGVALLPPLIS---ETSEWSTVYAKISGCSAMDSQALVRLRGSEAEILA 304  
 309 LSQKTSFTRVVDGAFEPNEPDLISQKPKAIPTITGVNNECGFLPMKEAPELSSG 368  
 305 INKVRKMPDAVVDGEFFPHPKELLASEDFHVPSTIIGVNDPEFGWIP-----VWMS 358  
 369 N---KSLMLHLONLH-----IPROYLHVANVYFPHDKSLYEIRSLDLIDGVDF 418  
 359 AQMIGITRENIQAVLKDTAVQOMLPPEBSSDLMEYEGDTEADQTLQITFEMGDMF 418  
 419 VVPALITARYHDAGAPVYFEFRHRPQCFEDTKPAFVADADAEVFEFGCAF--LKGD 476  
 419 VLPALQVAFOR--SHAPVYFEFRHPSYKQVPRPVADADAEVFEFGCAF--LKGD 477  
 478 F-----TEEEELLSRMMKYANFARHGNPNSEGLPYVPVMDHDEQYQLDIIQPAVGRA 531  
 537 LKEPRVDFTSTIP---LLISASDMLHSL 563  
 532 LKAGRLQFWTKTLPKRIQELKASQDGRRL 561

RESULT 10  
 Q8BK48 PRELIMINARY; PRT; 559 AA.  
 AC Q8BK48; 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,  
 RIKEN full-length enriched library, clone:503145B19 product:similar  
 to CARBOXYLESTERASE (EC 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE)  
 (MONOBUYTRASE) (COCAINE ESTERASE) (PROCAINE ESTERASE) (METHYLBUTYRASE)  
 (9030624L02Rik;)  
 GN Name:9030624L02Rik;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning."  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;  
 RA The FANTOM Consortium,  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes."  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Saeki N., Carninci P.,  
 Kono H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,  
 Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 Yoneda Y., Ishikawa K., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 Okazaki Y., Muramatsu M., Inoue I., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multichipillary sequencer."  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
 Kurihara C., Matsumoto H., Miyazaki A., Murata M., Nakamura M.,  
 Nishi K., Nomura K., Numazaki R., Ohno M., Ohse N., Okazaki Y.,  
 Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sato H.,  
 Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,  
 Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RT Submitted (Apr-2002) to the EMBL/Genbank/DBCP databases.  
 RL [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
 Altchul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.S., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kesteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman A.C., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzyaniak M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Maira M.A.,  
 RT Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.",  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 DR EMBL; AK077248; BAC6707.1; -.  
 DR EMBL; BC055062; AAH55062.1; -.  
 DR HSSP; P12337; 1k4Y.  
 DR MGI; 2443170; 9030624L02Rik.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR InterPro; IPR002018; CarboxylesteraseB.  
 DR InterPro; IPR000379; Ser\_ests.  
 DR Pfam; PF00135; Coesterase\_1.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Hydrolyase.

Query Match 559 AA; 62317 MW; CC14C61034A122C3 CRC64;

Best Local Similarity 48.7%; Score 1281; DB 2; Length 559;  
 Matches 260; Conservative 79; Mismatches 165; Indels 30; Gaps 8;

31 GBAEGBQNTLRGLTQKQVTVLGSPPVNVFLGPPFAPPLGSLRTNQPSVNDL 90  
 26 GDSASPIRNTHTGVRGSLVHVKTDLAVHTFLGIPAKPVGGLRPAPEADEPMSGV 85  
 91 REATSYPNCLQNSEML-LLDQMLKVHYPKRGVSEDCLYINITYAPAHADTGSCLPV 149  
 86 RGTGTHPMKCLQNDMLMGSEDLKMMNLILPISMSEDCLYINITYAPAHAGSNLPMVM 145  
 150 FPGGAFKTSASIFDGSALAAVEDLVVVOYRIGIFGFTTNDQAHGMAFKDQVAL 209  
 146 IHGGLTVMASMYDGSMLAATEDVVAIYRIGVGFSTGQVAKGNGWGLDQVAL 205  
 210 SWQKNIIEFGGDSSTVTFESAGATSVSSLLISPMKGLFKHAIMESGVALIIPYLEAH 269  
 206 RMVQNIHFGGNDPRVTTFESAGTSSVSHVSPMSQGLFGLAIMESGVALIPDLIS 265  
 270 DYKSEDLQVVAHFCGNNASDEALRLCLRTKPSKELLTISQTKGFTRVVDGAFPEMP 329  
 266 SSEWVH--RIYANLSGCAVNSEITLMGCLLKGKNAEMLINKVFKIIPGVNGEFLPKRP 323  
 330 LDLSQAFKAIPIIGVNNHEGFLIP-----MKEAPEILSGSNKSLALHL 376  
 324 QELMASDFFPVSIIIGINNDYGMILPTIMPAQRIEITRTKILPAVL-----KSTALMK 379  
 377 IQNLIHLPQYLHIVANEYFHDGSLTEIRDSLLDLGDFVFPVVALITARYHDAGAPV 436  
 380 M-----LPRECGDLMEETWGDTEDEPTIQAOFRKMGDFEVLPAQVAFHQR-SHAPV 433  
 437 YVEYFHRHQQCEBDTPAFVAKADHAEVAFVFGAFLKGDIVMEFGATEEKEKLSRGMK 496  
 434 YVEYFHRHQQCEBDTPAFVAKADHAEVAFVFGAFLKGDIVMEFGATEEKEKLSRGMK 496  
 497 YVATFARTGNPNDLSLMPAYNLTEOYLOLDLMSLQGLKEPRVDFWSTTP 550  
 490 YVANFARHGNPNSBGLPYMPVWHDHDOYLDLQDIPSVGRALKARLQFWTKTLP 543

RESULT 11  
 035533

ID 035533 PRELIMINARY; PRT; 559 AA.  
 AC 035533;  
 DT 01-JAN-1998 (TrEMBLrel. 05. Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05. Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26. Last annotation update)  
 DE Carboxylesterase precursor (EC 3.1.1.1).  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Syrian golden; TISSUE=Liver;  
 RA Some T., Wang C.Y.;  
 RT "Microsomal amidases and carboxylesterases";  
 RL (In) Guengerich F.P. (eds.);  
 RL COMPREHENSIVE TOXICOLOGY VOLUME 3, Biotransformation, pp.265-281,  
 RN Pergamon, Oxford (1997).  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Syrian golden; TISSUE=Liver;  
 RA Some T., Ishida Y., Takabatake E., Wang C., Isebe M.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 DR EMBL; D50577; BAA23605.1; -.  
 DR HSSP; P12337; 1k4Y.  
 DR CO; GO:0004091; F:carboxylesterase activity; IEA.  
 DR GO; GO:0016787; F:hydrolyase activity; IEA.  
 DR InterPro; IPR002018; CarboxylesteraseB.  
 DR InterPro; IPR000886; ER\_target\_S.  
 DR InterPro; IPR000379; Ser\_ests.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Hydrolyase; Signal.  
 FT SIGNAL 1 27 Potential.  
 FT CHAIN 28 559 carboxylesterase.  
 SQ SEQUENCE 559 AA; 62126 MW; 5B6BD4F9A47C6AD8 CRC64;

Query Match 41.5%; Score 1276.5; DB 2; Length 559;  
 Best Local Similarity 49.6%; Pred. No. 9.2e-89;  
 Matches 262; Conservative 79; Mismatches 172; Indels 15; Gaps 9;

28 GKTGPSABGPQNTLRGLTQKQVTVLGSPPVNVFLGPPFAPPLGSLRTNQPSVNDL 87  
 26 GDSASPIRNTHTGVRGSLVHVKTDLAVHTFLGIPAKPVGGLRPAPEADEPMSGV 82  
 88 DNREATSYPNCLQNSEMLLD-QHMLKVHYPKRGVSEDCLYINITYAPAHADTGSCLPV 146  
 83 SGVQDNISFPAMCLQNDMMNSSEGLKMKILMPISMSEDCLYINITYAPAHAGSNLPMV 142  
 147 LWFPGGAFKTSASIFDGSALAAVEDLVVVOYRIGIFGFTTNDQAHGMAFKDQVAL 206  
 143 IHGGLTVMASMYDGSMLAATEDVVAIYRIGVGFSTGQVAKGNGWGLDQVAL 202  
 207 AALSWQKNIIEFGGDSSTVTFESAGATSVSSLLISPMKGLFKHAIMESGVALIIPYLEAH 266  
 203 RMVQNIHFGGNDPRVTTFESAGTSSVSHVSPMSQGLFGLAIMESGVALIPDLIS 262  
 267 EANDYKSEDLQVVAHFCGNNASDEALRLCLRTKPSKELLTISQTKGFTRVVDGAFPEMP 326  
 263 SSEWVH--YTIYANLSDCAVNSEITLMGCLLKGKNAEMLINKVFKIIPGVNGEFLPKRP 320  
 327 NEPLDLSQAFKAIPIIGVNNHEGFLIP-----MKEAPEILSGSNKSL--AHLQNLILH 382  
 321 KHPQELLASADFFPVSIIIGVNNDEYGMILPVIMSGAQIKITRTVTLPAIKSTANQMK 380  
 383 IPPQYLHIVANEYFHDGSLTEIRDSLLDLGDFVFPVVALITARYHDAGAPVYFEFR 442  
 381 LPRECGDLMEETWGDTEDEPTIQAOFRKMGDFEVLPAQVAFHQR-AHAPVYFEFR 439  
 443 HRQCEBDTPAFVAKADHAEVAFVFGAFLKGDIVMEFGATEEKEKLSRGMKMTATPA 502



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Db 440 HRPSEFKTKPPHYADHGDSEFFVFVGN-LICG--IKF-ASTEERELLRSKQMKYANFA 495
Oy 503 RTGPNNGDLSLWPAVYNTEOYLQDLNMSLGRKLEKRPVDFWSTIP 550
Db 496 RHGNPNSNLPYPMLDHDEQYLOLDIKPAVGRALKARRLOFWTKILP 543

RESULT 12
OQB97 PRELIMINARY; PRT: 559 AA.
ID OQB97 01-MAR-2003 (TRENBLrel. 23, Created)
AC OQB97 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Mus musculus adult male colon CDNA, RIKEN full-length enriched
DE library, clone:9030624L02 product:similar to CARBOXYL ESTERASE (EC
DE 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE).
DE (PROCAINE ESTERASE) (METHYLBUTYRASE).
DE Name:9030624L02Rik;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=21085660; Pubmed=11217851; DOI=10.1038/35055500;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RA The PANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=20499374; Pubmed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kanno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=20530913; Pubmed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuana T., Teshiro H., Itoh M.,
RA Suni N., Iehi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Tanaka T., Kawanishi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

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RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imocani K., Iehi Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lyase family.
DR EMBL; AK033563; BAC28361.1; -.
DR HSSP; P12337; 1K4Y.
DR MCD; MG1.2443170; 9030624L02Rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000379; Ser_gestr.
DR InterPro; IPR00135; Coesterase; 1.
DR Pfam; PF00122; CARBOXYL ESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYL ESTERASE_B_2; 1.
DR KX Hydrolyase.
SQ SEQUENCE 559 AA; 62305 MW; 8C54D21522C52C4 CRC64;

Query Match 41.3%; Score 1271; DB 2; Length 559;
Best Local Similarity 48.7%; Pred. No. 2,4e-88;
Matches 260; Conservative 78; Mismatches 166; Indels 30; Gaps 8;

Oy 31 GPSAEGPQRNRLGKQKQYTVLGSPPVNVFVGPAPAPLGLSRTFNQGPSPMNTL 90
Db 26 QGDASPIRNTHTQVQSLVHVDTDAVHTFGIPAKPVPGLRAPPEADPEPMSGV 85
Oy 91 REATSYPLCLQNSEML-LDQHLKHYPKFVSEDCLYNTIYAPAHADTGSKLPLVLM 149
Db 86 RDGTSHPMLQNDMLNGSEBLKRMNLLIPISSEDCLYNTIYAPAHAGSNLPVVM 145
Oy 150 PFGAFKTSATIFDGSALAAVEDLVVVVQYRLGIFGFTTQDHPAGNAPYDQVAL 209
Db 146 IHGALTVGNASWYDGSMLATATEDVVVAIQYRLGVLFSTGDQAHAGNMGYLDQVAL 205
Oy 210 SWQKNTIEFGDSSVTITRESNGAISVSLISPPAKGLFHKALINESGVAIIPYLEAH 269
Db 206 RWOQONTVHFGNDRYITFESAGTSVSSHVSPMSQGFHAGINESGVAIIPDLISS 265
Oy 270 DYKSEBDLVYAHCGNNSSEALLRLCRTPKSEKLLTSOKTYSFTRVVDGAFPPNP 329
Db 266 SSEVNH-RIVANSGCAVASETLMLCKRGKMEMLAIKVKKIIPGVVDGEFLPNP 323
Oy 330 LDLSOKAFKAPSIIGVNNHCEGFLP-----MKAPETLSGSNKSALHL 376
Db 324 QELMASDQFHVPPIIGINDVEYMLPTIMDPQKIEIRKTLPAVL-----KSTALKM 379
Oy 377 IONTLHIPPQYLHVANEYFHDKSLIRIDSLDLGLGVFPVVPALITAYHNDAGPV 436
Db 380 M-----LPPECGLDIMEBYMDTEDPETLQAFREMKDFEVVPAIQVAFQR-SHAPV 433
Oy 437 YFEFRRHQCEFDTKAPFADHAEVRFVGGAPLKGDIWMEGATESEKLSRKMKK 496
Db 434 YFEFQHRPSFKQFRPYVADHDEFLVFGQF--GNKL--PYTEEEQLSRMKK 489
Oy 497 YMATFARTGNNGDLSLWPAVYNTEOYLQDLNMSLGRKLEKRPVDFWSTIP 550
Db 490 YRAFPARHGNNSGSLPYPMVDHDEQYLOLDIKPAVGRALKARRLOFWTKILP 543

RESULT 13
OQB97 PRELIMINARY; PRT: 556 AA.
ID OQB97 05-JUL-2004 (TRENBLrel. 27, Created)
AC OQB97 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein BC015286.

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GN Name=BC015286;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Kleene R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stempleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
RA Richards S., Worley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Young A.C., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN 12;
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RX Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/11pase family.
DR EMBL: BC058815; AAH58815.1; -.
DR HSSP: P12337; 1K4Y.
DR GO: GO:0016787; F:hydrolyase activity; IEA.
DR InterPro: IPR002018; Carboxylesterase.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KM Hydrolase; Hypothetical protein.
SQ
SEQUENCE 556 AA; 61927 MW; 58DE05A3C73BECD CRC64;

Query Match 41.1%; Score 1266.5; DB 2; Length 556;
Best Local Similarity 47.1%; Pred. No. 5.3e-88;
Matches 273; Conservative 76; Mismatches 190; Indels 41; Gaps 12;

QY 1 MPQGLTSSASQWCFLL--LQPLLGRHOMKGTGPSAEGRQKTRIGLWIGKQVTVLGSPPV 58
DB 1 MPR---SQMHNWLDVLLFGILLLLGHVQ-GQDSPEA-SPIRRTHTGQVAGSLVHKOTKA 55
QY PVNVFGLGVPRAAPPLGLRFTNPQSPMDNIREATSYNLCLONSEWMLLDQMLKXHY 118
DB 56 GYHTFLGDIIPRAKPPVGPRLRAPPEAPEPWSGVDRDTAHPAMCLQ-----LGMKEIKKL 111
QY 119 PKFGVSEDCLYINITYAPAHADTGSKLPLVWFGAFTGSASTFDGALAAVSDVLVVV 178
DB 112 PAVSTSEDCLYINITYAPAHAGSNLPLVWVTHGGGLVAGNAAVSDGSLIAAIDLVVVT 171
QY 179 VQYRIGIFGFPTTQOHAFGNMAFQDVAALSWQKNIEFGGSPSSVTIFGSSAGALSY 238
DB 172 IQYRIGVGLGFSTGQOHAGNMGFLDQVAALRWIQNLAHNGGGRDVTITFGSAGGTSV 231
QY 239 SSLISPAKGLFHKAIMESGVALIPYLEADHYEKSELDQVVAHFCCNNADEALLRCL 298
DB 232 SSHVVSPPMSKGLFHAIMESGVALIPYLTITSSMS--TTVAKLSCCEAMDEALLRCL 269
QY 269 RTKPSKELLTISQKTKSTRVYVDAFAFPNEDLISQAKFAKPSITIGVNNHCGSLM 358
DB 290 RGSBAELTALAKLVQMIPAVVDEFPFPRPKELLASEDPHPVPSITIGVNNHCGSLM 348

GN Name=BC015286;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Kleene R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stempleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
RA Richards S., Worley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Young A.C., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN 12;
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RX Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/11pase family.
DR EMBL: BC074230; AAH74230.1; -.
KM Hydrolase; Hypothetical protein.
SQ
SEQUENCE 556 AA; 61927 MW; 58DE05A3C73BECD CRC64;

Query Match 41.1%; Score 1266.5; DB 2; Length 556;
Best Local Similarity 47.1%; Pred. No. 5.3e-88;
Matches 273; Conservative 76; Mismatches 190; Indels 41; Gaps 12;

QY 1 MPQGLTSSASQWCFLL--LQPLLGRHOMKGTGPSAEGRQKTRIGLWIGKQVTVLGSPPV 58
DB 1 MPR---SQMHNWLDVLLFGILLLLGHVQ-GQDSPEA-SPIRRTHTGQVAGSLVHKOTKA 55
QY PVNVFGLGVPRAAPPLGLRFTNPQSPMDNIREATSYNLCLONSEWMLLDQMLKXHY 118
DB 56 GYHTFLGDIIPRAKPPVGPRLRAPPEAPEPWSGVDRDTAHPAMCLQ-----LGMKEIKKL 111
QY 119 PKFGVSEDCLYINITYAPAHADTGSKLPLVWFGAFTGSASTFDGALAAVSDVLVVV 178
DB 112 PAVSTSEDCLYINITYAPAHAGSNLPLVWVTHGGGLVAGNAAVSDGSLIAAIDLVVVT 171
QY 179 VQYRIGIFGFPTTQOHAFGNMAFQDVAALSWQKNIEFGGSPSSVTIFGSSAGALSY 238
DB 172 IQYRIGVGLGFSTGQOHAGNMGFLDQVAALRWIQNLAHNGGGRDVTITFGSAGGTSV 231
QY 239 SSLISPAKGLFHKAIMESGVALIPYLEADHYEKSELDQVVAHFCCNNADEALLRCL 298
DB 232 SSHVVSPPMSKGLFHAIMESGVALIPYLTITSSMS--TTVAKLSCCEAMDEALLRCL 269
QY 269 RTKPSKELLTISQKTKSTRVYVDAFAFPNEDLISQAKFAKPSITIGVNNHCGSLM 358
DB 290 RGSBAELTALAKLVQMIPAVVDEFPFPRPKELLASEDPHPVPSITIGVNNHCGSLM 348

RESULT 14
ID O6GM54 PRELIMINARY; PRT; 568 AA.
AC O6GM54;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE LOC443703 protein (Fragment).
GN Name=LOC443703;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OX Xenopodinae; Xenopus.
NCBI_TaxID=8355;
RN 11;
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Kleene R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stempleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
RA Richards S., Worley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Young A.C., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN 12;
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Dev. Dyn. 225:384-391(2002).
RN 13;
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/11pase family.
DR EMBL: BC074230; AAH74230.1; -.
KM Hydrolase activity; IEA.

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DR InterPro: IPR002018; CarboxylesteraseB.  
 DR InterPro: IPR000379; Ser\_estrs.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 DR Hydrolyase.  
 KM Hydrolyase.  
 FT NON\_TER  
 SQ SEQUENCE 568 AA; 63032 MW; 93360B6B53931A1 CRC64;

Query Match 41.0%; Score 1263.5; DB 2; Length 568;  
 Best Local Similarity 48.2%; Pred. No. 9.2e-88;  
 Matches 258; Conservative 87; Mismatches 169; Indels 21; Gaps 8;

QY 28 GKTGSAEGPQNRTRIGWVIGKQVTVLGSPPVNVFLGVPAPPLGSLRFTNPQSPW 87  
 DB 28 GYGTEDARPLLTITVYGGGLGKTGKATDRILIHFMGVFAKPRIGLRFEDPDQPEW 87  
 QY 88 DNLRATSYDNLCLQNSEWL--LDDQHLKHYPRFGVSEDCLYNITAPAHADTGSKL 145  
 DB 88 SSIREATENPWCLODKKMEQLADFFKAKFPDP--VSEDCLYNITVFPADRGENPELP 145  
 QY 146 VLVMPFGAFTGSAIFDGSALAAVEDLVVVVVOYRIGIFGPFITWDHAGNNAFKQ 205  
 DB 146 VNVFTHGGGLTGMAGMEBSALSAVENVVVSIQRIIGMGPFTGDKKAGNNGFLDQ 205  
 QY 206 VVALSMVQKNIIEFGSDPSSVTIIFGESAGAISSSLISPMKGFPHKAIMESGVALIPY 265  
 DB 206 VVALSMVQKNIIEFGSDPSSVTIIFGESAGAISSSLISPMKGFPHKAIMESGVALIPY 265  
 QY 266 LEANDYKESDQVVAHFCCGNASDS--EALLRCLRTKPSKELLTTSQKTK--SFTRVVDG 322  
 DB 266 LMA---SKTEKILPIHVAANTSSCSVSLADCLKKTEDEIVAIISAAMKFAVFAVVDG 322  
 QY 322 AAPPHEPDLISQKAFKAPSIIGVNNHCGFLPMPKEAPELLSGNSKSLALHLIONILH 382  
 DB 322 VFLPRAEELIASKSNPVPFLIGVNNHFGWILPALN--ISGRSEMEKDDIQSLIV 379  
 QY 382 IPPQYLH-----LVANEYFHDKSLTEIRSDLSLDLGDVFPVVPALITARYHDAGAP 435  
 DB 382 ALP-FVHSTSVVPIIMEYFGDTNDPKLRNNPFLDVLVDIIFVLPALRTAKYHDSGR 438  
 QY 436 VYFEFRHRPQCFEDTKPAFVKAHDAEVRVFGAFKLGDIWMEGATEEESKLLSRKM 495  
 DB 436 VYFEFRHRPQCFEDTKPAFVKAHDAEVRVFGAFKLGDIWMEGATEEESKLLSRKM 495  
 QY 495 KVMATPARNGNNDLSMPAYNLTEOYLQDLNMSLQGLRKEPRVDWTSTIP 550  
 DB 495 KVMATPARNGNNDLSMPAYNLTEOYLQDLNMSLQGLRKEPRVDWTSTIP 550  
 QY 550 KVMATPARNGNNDLSMPAYNLTEOYLQDLNMSLQGLRKEPRVDWTSTIP 550  
 DB 550 KVMATPARNGNNDLSMPAYNLTEOYLQDLNMSLQGLRKEPRVDWTSTIP 550

## RESULT 15

070177 PRELIMINARY; PRT; 561 AA.

ID 070177  
 AC 070177  
 DT 01-AUG-1998 (TRMBLrel. 07, Created)  
 DT 01-AUG-1998 (TRMBLrel. 07, Last sequence update)  
 DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)  
 DE Carboxylesterase precursor (EC 3.1.1.1).  
 GN Name=carboxylesterase;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RP STRAIN=Miscar; TISSUE=Small intestine;  
 RA Sone T., Kunikomo T., Isebe M.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY. Belongs to the type-B carboxylesterase/lipase family.  
 DR EMBL; AB010632; BAA25691.1; -.  
 DR HSSP; P37967; I0E3.  
 DR GO; GO:0004091; F:carboxylesterase activity; IEA.  
 DR GO; GO:0016787; F:hydrolyase activity; IEA.

DR InterPro: IPR002018; CarboxylesteraseB.  
 DR InterPro: IPR000379; Ser\_eastr.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 DR Hydrolyase; Signal.  
 KM Hydrolyase; Signal.  
 FT SIGNAL  
 FT CHAIN  
 SQ SEQUENCE 561 AA; 62239 MW; 73A468C3F96939B CRC64;

Query Match 41.0%; Score 1262.5; DB 2; Length 561;  
 Best Local Similarity 48.8%; Pred. No. 1.1e-87;  
 Matches 275; Conservative 77; Mismatches 179; Indels 33; Gaps 13;

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 DB 1 MPRNQLHSMANLVLEGLL--LLIHVQ--GQSSPES--SIRRTHTGQVQKLDHVDYTAG 56  
 QY 60 VNVFLGVPAPPLGSLRFTNPQSPWPDNIREATSYDNLCLQNSEWL--LDDQHLK 115  
 DB 57 VHTFLGIPFAKPPVGPLRFAPPEPEPWSGVADATSQPAMCLONDIIDEVGLDMKMI- 115  
 QY 116 VHYPRGVSIEDCLYNITAPAHADTGSKLPLYVMPFGAFTGSAIFDGSALAAVEDLV 175  
 DB 116 --LSSISMSIEDCLYNITAPAHAREGSLPVVWVTHGALLVGMASMTDGLITVNEEDLV 173  
 QY 176 VVVVOYRIGIFGFTTPOHAPGNMAFKDQVAAALSMVQKNIIEFGSDPSSVTIIFGESAGA 235  
 DB 174 VVTIYRIGVLCGFSTGEBHARGWGYLDQVALLRMVQONIAHFGCNRRVYIIFESAGG 233  
 QY 236 ISVSSSLISPMKGFPHKAIMESGVALIPYLEANDYKESDQ--VVAHFCCGNASDSAL 294  
 DB 234 TSVSHVSLSPMSQGLFHGAIMESGVALIPDLIS--ETSFTVSTVAKLSGCEANDSEAL 290  
 QY 295 LRCLRTKPSKELLTTSQKTKSTRVVDGAFPPNEEDLSQKAFKAPSIIGVNNHCGFL 354  
 DB 291 VRCIRAKSGAETLVNKKVFKMIPAVVDGEFLPRHKEILLASEDFHPVPSIIIGNTDEYCC 350  
 QY 355 LLPM-----KEAPELISGNSKSLALHLIONILHIPQYLHLVANEYFHDKSLTEIR 406  
 DB 351 TIPIWMGTQRIKE-----LSRENDAVLKDTAAGMMLPECGDILLMEYMGNTDSSQTLQ 406  
 QY 407 DSLDLGLGDVFPVVPALITARYHDAGAPVYFEFRHRPQCFEDTKPAFVKAHDAEVR 466  
 DB 407 IQYTEMGDPLFVILQVAHFQR--SHAPVYFEFOHAPSYFKVNRPPHYADHDAEVPF 465  
 QY 467 VFGAFKLGDIWMEGATEEESKLLSRKMKYATATARGNPNNDLSMPAYNLTEOYLQ 526  
 DB 466 VF-GSFPFGMKLDF--TEEBRLSRMKYANFARQNPSEGLPYMPALDHDEOYLQ 521  
 QY 527 LDNMSLQGLRKEPRVDWTSTIP 550  
 DB 522 LDTHPAVDALAKRRLOFWTKLP 545

Search completed: June 16, 2005, 20:44:57  
 Job time : 183 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 20:31:14 ; Search time 42 Seconds  
(without alignments)  
1032.645 Million cell updates/sec

Title: US-10-674-636-2

Perfect score: 3079

Sequence: 1 MPQGLTSSASQWCFLLIOP.....PLSLTFLSLQPPFFCAP 581

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
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6: /cgn2\_6/ptodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	3079	100.0	US-10-023-515-2	Sequence 2, Appli
2	1230	39.9	US-09-595-682B-28	Sequence 28, Appli
3	1230	39.9	US-09-949-016-6426	Sequence 6426, Ap
4	1230	39.9	US-09-949-016-9670	Sequence 9670, Ap
5	1150.5	37.4	US-09-595-682B-21	Sequence 21, Appli
6	1138.5	37.0	US-09-264-737-2	Sequence 2, Appli
7	1130.5	36.7	US-09-595-682B-26	Sequence 26, Appli
8	1091.5	35.4	US-08-845-295A-2	Sequence 2, Appli
9	1091.5	35.4	US-09-140-933-2	Sequence 2, Appli
10	1091.5	35.4	US-09-146-661-2	Sequence 2, Appli
11	1091.5	35.4	US-09-150-515-2	Sequence 2, Appli
12	1034.5	33.6	US-09-264-737-1	Sequence 1, Appli
13	942.5	30.6	US-08-446-100-26	Sequence 26, Appli
14	942.5	30.6	US-08-446-100-28	Sequence 28, Appli
15	942.5	30.6	US-08-446-100-30	Sequence 30, Appli
16	942.5	30.6	US-08-446-100-31	Sequence 31, Appli
17	940.5	30.5	US-08-446-100-27	Sequence 27, Appli
18	940.5	30.5	US-08-446-100-29	Sequence 29, Appli
19	871	28.3	US-10-023-515-4	Sequence 4, Appli
20	793	25.8	US-09-949-016-8386	Sequence 8386, Ap
21	786	25.5	US-09-949-016-6888	Sequence 6888, Ap
22	782	25.4	US-09-949-016-8387	Sequence 8387, Ap
23	777.5	25.3	US-09-491-356C-20	Sequence 20, Appli
24	777	25.2	US-08-348-920-1	Sequence 1, Appli
25	775	25.2	US-09-491-356C-23	Sequence 23, Appli
26	774	25.1	US-08-348-920-2	Sequence 2, Appli
27	772	25.1	US-09-491-356C-22	Sequence 22, Appli

28	769	25.0	836	4	US-09-491-356C-21	Sequence 21, Appli
29	765.5	24.9	614	3	US-08-446-100-25	Sequence 25, Appli
30	764.5	24.8	614	1	US-07-732-962A-2	Sequence 2, Appli
31	764.5	24.8	614	2	US-08-370-156-2	Sequence 2, Appli
32	764.5	24.8	614	3	US-08-446-100-19	Sequence 19, Appli
33	764.5	24.8	614	3	US-08-446-100-21	Sequence 21, Appli
34	764.5	24.8	614	3	US-08-814-095-2	Sequence 2, Appli
35	764.5	24.8	614	5	PCT-US92-06106-2	Sequence 2, Appli
36	764.5	24.8	645	4	US-09-949-016-7063	Sequence 7063, Ap
37	764.5	24.8	645	4	US-09-949-016-7064	Sequence 7064, Ap
38	762.5	24.8	614	3	US-08-446-100-20	Sequence 20, Appli
39	761.5	24.7	614	3	US-08-446-100-23	Sequence 23, Appli
40	760.5	24.7	614	3	US-08-446-100-22	Sequence 22, Appli
41	759.5	24.7	600	2	US-08-370-156-4	Sequence 4, Appli
42	759.5	24.7	600	3	US-08-814-095-4	Sequence 4, Appli
43	759.5	24.7	600	3	US-08-975-084-1	Sequence 1, Appli
44	755.5	24.5	617	2	US-08-370-156-6	Sequence 6, Appli
45	755.5	24.5	617	3	US-08-814-095-6	Sequence 6, Appli

## ALIGNMENTS

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RESULT 1
US-10-023-515-2
; Sequence 2, Application US/10023515
; Patent No. 6664091
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYL ESTERASE
; FILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/023,515
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,369
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-515-2
Query Match 100.0%; Score 3079; DB 4; Length 581;
Beet Local Similarity 100.0%; Pred. No. 0;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPQGLTSSASQWCFLLIOPLLGHROWKTPSASGPOBNRLGMIQKQVTVGSPVPV 60
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QY 61 NVFLGVPAAPPLGSLRFTNPQSPASPMNDLREATSYNLCIONSEWLLDQMLKVHPK 120
DB 61 NVFLGVPAAPPLGSLRFTNPQSPASPMNDLREATSYNLCIONSEWLLDQMLKVHPK 120
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DB 121 FGVEDCLYNTIYAPAHADTGSKLPLVLPFGGAFKTSASIFPGSALAAVEDLVVVVQ 180
QY 121 FGVEDCLYNTIYAPAHADTGSKLPLVLPFGGAFKTSASIFPGSALAAVEDLVVVVQ 180
DB 121 FGVEDCLYNTIYAPAHADTGSKLPLVLPFGGAFKTSASIFPGSALAAVEDLVVVVQ 180
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DB 181 YRLGIPFTTWDHAGNNAFKQVVALSVQKNIEFGSDPSVTIFGSAGASIVSS 240
QY 181 YRLGIPFTTWDHAGNNAFKQVVALSVQKNIEFGSDPSVTIFGSAGASIVSS 240
DB 181 YRLGIPFTTWDHAGNNAFKQVVALSVQKNIEFGSDPSVTIFGSAGASIVSS 240
QY 241 LILSPMAKGLFHKAIMESGVALIIFLEAHDYKSESDQVAHFCGNNASDEALLRCIRT 300
DB 241 LILSPMAKGLFHKAIMESGVALIIFLEAHDYKSESDQVAHFCGNNASDEALLRCIRT 300
QY 301 KPSSELLTTSOKTYSFTRVVDGAFPNEDLLSQKPAKAIPIITGVNNECGFLPMKE 360
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Db 301 KPSKELTLOSQKTSFTRVVDGAFENEPDLDSQKAFKAPSIIGVNNHCGFLPME 360  
 Qy 361 APETLSGNSKSLAHLIIONILHIPPQYLHVANEYFDKSLTEIRDSLLDLGDVFFV 420  
 Db 361 APETLSGNSKSLAHLIIONILHIPPQYLHVANEYFDKSLTEIRDSLLDLGDVFFV 420  
 Qy 421 PALITARYHRGAGPVYFEFRHRPOCFEDTKPAFYKADHADVRFVFGAFLKGDIVMF 480  
 Db 421 PALITARYHRGAGPVYFEFRHRPOCFEDTKPAFYKADHADVRFVFGAFLKGDIVMF 480  
 Qy 481 EGATEEKLISRKKMKYATFAARTGNPNDLSLMPAYNLTEOYLQDLNMSLQRLKEP 540  
 Db 481 EGATEEKLISRKKMKYATFAARTGNPNDLSLMPAYNLTEOYLQDLNMSLQRLKEP 540  
 Qy 541 RYDFMTSTIPLISASDMLSPSSITFSLLOPFFFCAP 581  
 Db 541 RYDFMTSTIPLISASDMLSPSSITFSLLOPFFFCAP 581

RESULT 2  
 US-09-595-682B-28  
 / Sequence 28, Application US/09595682B  
 / Patent No. 6800483  
 / GENERAL INFORMATION:  
 / APPLICANT: Danke, Mary K.  
 / APPLICANT: Potter, Philip M.  
 / APPLICANT: Houghton, Peter J.  
 / TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of  
 / FILE REFERENCE: SJ-0005  
 / CURRENT APPLICATION NUMBER: US/09/595, 682B  
 / PRIOR FILING DATE: 2000-01-16  
 / PRIOR APPLICATION NUMBER: 60/075,258  
 / PRIOR FILING DATE: 1998-02-19  
 / PRIOR APPLICATION NUMBER: PCR/US99/03171  
 / NUMBER OF SEQ ID NOS: 30  
 / SOFTWARE: PatentIn Ver. 2.0  
 / SEQ ID NO 28  
 / LENGTH: 559  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 US-09-595-682B-28

Query Match 39.9%; Score 1230; DB 4; Length 559;  
 Best Local Similarity 46.7%; Pred. No. 4.8e-125;  
 Matches 248; Conservative 91; Mismatches 168; Indels 24; Gaps 8;  
 Qy 31 GPSAEGPQNTRLGMIQKQVTVLGSVPVNVFLGVFPAPPLGSLRFTNPOPASPMWNL 90  
 Db 26 GQDSASEIRTHTGQVLSLVHVKGNAGVQTFGLGIPFAKPLGLRFAPEPPESMGV 85  
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 Db 86 RDGTHPACLODLTAVESEFL-----SQFNMTFPDSMSDECLYISTTPAHSHSGSNLP 141  
 Qy 146 VLVWFGGAFKTKGSASIFDGSALAAVEDLVVVVVOYRLGIFGFTTMDQAHGNNWAFDQ 205  
 Db 142 VWWHIGGLVVGMSLVDGSMALLENVVVYIYRLGVLGFFSTGDKHATGMMGYLDQ 201  
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 Db 202 VVALSVQKNIIEFGGDPSSVTIFGESAGAISVSSLLISPAKGLFKAHAIWESGVAIIIPY 265  
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 Db 262 LTA-----SSADVISIVVANLSACQDVSEBALVGLCRKSKKEILAIKPKFMIPGVVDG 317  
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 Db 378 FLPRHPQELASADQPVPSIVGNNHFGWILPKWRIYDTQKEMREASQALQKMLT 377  
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Db 378 LLMPPFGDLLEEBYIGDNGDPQTLQAOQFQEMADSMWVIRLQVANH-QCSRAVYF 436  
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 Db 437 EFRHRPOCFEDTKPAFYKADHADVRFVFGAFLKGDIVMFEGATEEKLISRKKMKY 499  
 Qy 500 TPARTGNPNDLSLMPAYNLTEOYLQDLNMSLQRLKEPVDPMWSTIP 550  
 Db 493 NFRANGPNNGEGLPHWPLFDQEEYOYLNLTQAVGRALKAHRLQWKAALP 543

RESULT 3  
 US-09-949-016-6426  
 / Sequence 6426, Application US/09949016  
 / Patent No. 6812339  
 / GENERAL INFORMATION:  
 / APPLICANT: VENTER, J. Craig et al.  
 / TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 / WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 / FILE REFERENCE: CL001307  
 / CURRENT APPLICATION NUMBER: US/09/949, 016  
 / PRIOR FILING DATE: 2000-04-14  
 / PRIOR APPLICATION NUMBER: 60/241,755  
 / PRIOR FILING DATE: 2000-10-20  
 / PRIOR APPLICATION NUMBER: 60/237,768  
 / PRIOR FILING DATE: 2000-10-03  
 / PRIOR APPLICATION NUMBER: 60/231,498  
 / PRIOR FILING DATE: 2000-09-08  
 / NUMBER OF SEQ ID NOS: 207012  
 / SOFTWARE: FastSeq for Windows Version 4.0  
 / SEQ ID NO 6426  
 / LENGTH: 559  
 / TYPE: PRT  
 / ORGANISM: Human  
 US-09-949-016-6426

Query Match 39.9%; Score 1230; DB 4; Length 559;  
 Best Local Similarity 46.7%; Pred. No. 4.8e-125;  
 Matches 248; Conservative 91; Mismatches 168; Indels 24; Gaps 8;  
 Qy 31 GPSAEGPQNTRLGMIQKQVTVLGSVPVNVFLGVFPAPPLGSLRFTNPOPASPMWNL 90  
 Db 26 GQDSASEIRTHTGQVLSLVHVKGNAGVQTFGLGIPFAKPLGLRFAPEPPESMGV 85  
 Qy 91 REATSYENCLQN-----SEWLLDQMLKVHPKGVSEDCLYINITYAPAHADTGSCLP 145  
 Db 86 RDGTHPACLODLTAVESEFL-----SQFNMTFPDSMSDECLYISTTPAHSHSGSNLP 141  
 Qy 146 VLVWFGGAFKTKGSASIFDGSALAAVEDLVVVVVOYRLGIFGFTTMDQAHGNNWAFDQ 205  
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 Db 262 LTA-----SSADVISIVVANLSACQDVSEBALVGLCRKSKKEILAIKPKFMIPGVVDG 317  
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 Qy 378 FLPRHPQELASADQPVPSIVGNNHFGWILPKWRIYDTQKEMREASQALQKMLT 377  
 Db 378 FLPRHPQELASADQPVPSIVGNNHFGWILPKWRIYDTQKEMREASQALQKMLT 377  
 Qy 440 EFRHRPOCFEDTKPAFYKADHADVRFVFGAFLKGDIVMFEGATEEKLISRKKMKY 499  
 Db 437 EFRHRPOCFEDTKPAFYKADHADVRFVFGAFLKGDIVMFEGATEEKLISRKKMKY 499

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QY 500 TPAATGNNGNDLSLMPAYNLTEOYLQDLNLSLQRLKEPRVDFWTSTIP 550
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US-09-949-016-9670
; Sequence 9670, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9670
; LENGTH: 577
; TYPE: PRF
; ORGANISM: Human
US-09-949-016-9670

Query Match 39.9%; Score 1230; DB 4; Length 577;
Best Local Similarity 46.7%; Pred. No. 5,1e-125;
Matches 248; Conservative 91; Mismatches 168; Indels 24; Gaps 8;

QY 31 GPSAEGPQNRRLGRTIOGQVTVLGSVPVNVFLGVPRAAPPLGSLRTNPOPAFMDL 90
Db 44 GODSASPIRTHHTGVLGSLVHVKGANGVOTFLGIPAKPPLGLRPAPEPPESWSGV 103
QY 91 REATSPMLCION-----SEWLLDQHLKHYHFKFVSEDCLYNTIYAPALADGSLKP 145
Db 104 RDGTHPMWCLODLTAVESSEFL----SQPNMTFEDSDSEDCLYSTTPAHSHGSLUP 159
QY 146 VLWVPGGAFKTSASIFDGSALAAVEDVLVVVVOYRLGIFGFTTMDQHAFGNNAFKDQ 205
Db 160 VVVVHGGALVFGMASLVDGSLALBNVYVYIIYRLGVLGFSTGDKHATGMVYLDQ 219
QY 206 VAALSVOKNIEFGGDPSSVTTFGESAGALSVSLLISPMAGLFFHKAIESGVAILPY 265
Db 220 VAALEWVOQNIAHFGANPDRAVTIFGESAGTSVSSLVVSPISQGLFHGAIMESGVALLPG 279
QY 266 LEAHYKESDL--QVNAHFGGNMNSDSEALLRCRTKPSKELLTLSQKTSFTTVUGA 323
Db 280 LIA----SSADVISTVIANLSACDQVDSBALVGCIRGSKKEITLAINKPPKMT PGVVDGV 335
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Db 336 FLPRHPQELLSADQPPPSITGVANNHFGWILIPYVMIYDTQKMDREASQAALQKMLT 395
QY 360 ILIHPYLIHIVANVEYFHDKSLTEIRDSLDDLDGVFFVVPALITARYHRDAGAPVYFY 439
Db 396 LLMLPPTFGDLIREYIGNGDPQTLQAOPQEMADSMFVILPALQVAF--QCSRAPVYFY 454
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Db 455 EFQHPSWLKNIRPHMKADHGDDELRFV--RSFEGGANIKF--TEEBEQSLRKMKKYWA 510
QY 500 TPAATGNNGNDLSLMPAYNLTEOYLQDLNLSLQRLKEPRVDFWTSTIP 550
Db 511 NFARNGNNGEGCLPHWPLFDQEEYQLQNLQPAVGRALKAHRLQFMKALP 561

RESULT 5
US-09-595-682B-21
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; Sequence 21, Application US/09595682B
; Patent No. 6800483
; GENERAL INFORMATION:
; APPLICANT: Danks, Mary K.
; APPLICANT: Potter, Philip M.
; APPLICANT: Houghton, Peter J.
; TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of
; FILE REFERENCE: SJ-0005
; CURRENT APPLICATION NUMBER: US/09/595,682B
; PRIOR FILING DATE: 2000-01-16
; PRIOR APPLICATION NUMBER: 60/075,258
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: PCT/US99/03171
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 565
; TYPE: PRF
; ORGANISM: Oryctolagus cuniculus
US-09-595-682B-21

Query Match 37.4%; Score 1150.5; DB 4; Length 565;
Best Local Similarity 43.9%; Pred. No. 2,5e-116;
Matches 252; Conservative 75; Mismatches 180; Indels 67; Gaps 13;

QY 12 WCFELIQLPLGHGHWGKTGPSAEGPQNRRLGRTIOGQVTVLGSVPVNVFLGVPFAAP 71
Db 2 WLCALALSLAAGTACWGH--PSAP-PVVDYHGVKVLGKFVSLBGFQAVAVFLGVFPAPK 58
QY 72 PLGSLRFTNPOPASPMNDLREATSPMLCIONSEWLLDQHL-----KVHYR-KKGV 123
Db 59 PLGSLRFPAPQPASWSHVKTTSYPPMCSQDA----VSGHMLSELFTNRKENIPLKE-- 112
QY 124 SEDCLYNTIYAPALADGSLKPLVTVWVPPGGAFTKGSASIFPGSALAAVEDVLVVVOYRL 183
Db 113 SEDCLYNTIYAPALDYLTKRGLPVVWVHGGALWGVASTYDGLLSAHENVVVYTTQRL 172
QY 184 GIFGFTTMDQHAQGNNAFKQVNAALSVOKNIEFGGDPSSVTTFGESAGALSVSLLT 243
Db 173 GIMGFSTGDSHSGNMGHLDQVNAALRVQDNIAHFGDPSSVTTFGESAGGOSVILL 232
QY 244 SPMAKGLFHKAIESGVAILPYLEAHYKESD--LQVNAHFGGNMNSDSEALLRCRTK 301
Db 223 SPLTKNLFHRAISGVALLSL-----FRKTKSLAEKIALBAGCKTTSVAVVHCLROK 288
QY 302 PSKELL--TLSOK-----TKSPTRVVDGAF FFPNEPLDLSQAKFAIPSIIG 346
Db 289 TEEBIMEVTLKMKFMAADLVGDPKENTAFITTVIDGVLLPAPAPAILAEKYNMLPYWVG 348
QY 347 VNNHCEGFLPM-----KEAPEILSGSNKSLALHLIONLHITPROYLHVA 392
Db 349 INOGEFGWILPMQWGLPPLSGKLDQKATLWMS-----YPLVANSKELTPAT 399
QY 393 NEYFHDKSLTEIRDSLDDLDGVFFVVPALITARYHRDAGAPVYFYEFRRPQCFEDTK 452
Db 400 EKLIGCTDDPKKCDLFLMDLADLLFGVPSVNAHRHDAGAPYMYEYRRPSSDMR 459
QY 453 PAFVADHAEVRVFGAFLKGDIVNEEGATEEELKLSRKMKKYWATPAATGNNGNDL 512
Db 460 PKTVIGDHGDEIFSLGAPFLK-----EGATEEELKLSKVMYKXWAFARNGNNGEGCL 513
QY 513 SLMPAYNLTEOYLQDLNLSLQRLKEPRVDFWT 546
Db 514 POWPAYDYKESYLOIGATTQAQKLKQKXVAFWT 547

RESULT 6
US-09-264-737-2
; Sequence 2, Application US/09264737A
; Patent No. 6107549
; GENERAL INFORMATION:
```



APPLICANT: Feng, Paul C.C.  
APPLICANT: Ruff, Thomas G.  
TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via  
TITLE OF INVENTION: Expression of Esterase Enzymes  
FILE REFERENCE: 38-21(10551) PLE3 Pyridine Tolerance  
CURRENT APPLICATION NUMBER: US/09/264,737A  
CURRENT FILING DATE: 1999-03-09  
EARLIER APPLICATION NUMBER: 60/077,377  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 566  
TYPE: PRT  
ORGANISM: Rabbit  
US-09-264-737-2

Query Match 37.0%; Score 1138.5; DB 3; Length 566;  
Best Local Similarity 43.6%; Pred. No. 5.1e-115;  
Matches 250; Conservative 75; Mismatches 176; Indels 73; Gaps 14;

QY 12 WCFELIQLPLGHRQMGKTPSABGFORNTLGMIOGKQVTVLGSPPVNVFLGVPFAAP 71  
DB 9 WLF-----IAACTAGH--PSAP--PVVDYVKGVLGKVFSLGFAQVAVFLGVPAKP 59  
QY 72 PLGSLRFTNPQAPSPMDNLRKATSYPNLCLNSEWLLDDQML-----KVHYP-KPGV 123  
DB 60 PLGSLRFAFPQAPAESHSVHKNTTSYPPWCSDA-----VSGHMLSELFTNRKENIPLKF-- 113  
QY 124 SEDCLYINLYAPAHADTSKLPVLVWFPFGAFKTPGASIFDGSALAAVEDLVVVOGYRL 183  
DB 114 SEDCLYINLYTPADLTKRGRLPVWVWVHGGGLMVGASTYDGLALSHENVVVTTIOYRL 173  
QY 184 GIGFETTTMDHAPQNMWAFKQOVAALSVQKNIFFPGDSSVTTFGESAGALSVSLL 243  
DB 174 GIGGFSTGDEHSRGNMCHLDQVAAALRWQDNINFGDPSYTFGESAGGSVSITLL 233  
QY 244 SPMAGLFHKAIMSGVAIIPYLEAHDYKSED--LQVVAHFCGNNADEBALLRCIRTK 301  
DB 234 SPLTKNLFHRAISSEGVALLSSL-----FRKNTSLAKIAIEAGCKTTTSAVWVHCLROK 289  
QY 302 PSKELL--TISQK-----TKSFTRVVDGAFPNNEBLDLSQKAFAPISITG 346  
DB 290 TEEELMEVTLKMKMALDVGDPRENTAFITTVIDGVLFPKAPAEILAEKKVMMLPYMG 349  
QY 347 VNNHECGFLPM-----KEAPEILSGNSKSLAHLIQLNIHIPPQYLAHA 392  
DB 350 INQOEFMIIIPMQLGYPLSEGLDKQKATLMLKS-----YPIVNSKELTPVAT 400  
QY 393 NEYHHDGSLTEIRDLSLDLIGVFFVVPALITARYHRDAGAVVYFYEPRHRPOCFEDTK 452  
DB 401 EKYIGCTDDPVKKKDLFLDMLADLLFGVPSVNVARHHRDAGAPTYVEYRVRPSSDMR 460  
QY 453 PAFVKADHADEVAFVFGAFLKGDIVMFEAGATEEELSRKMKKWATFARTGNNGNDL 512  
DB 461 PKTVIGDHGEIRSVLGAPFLK-----EGATEEELKLSKMKWAKWANFARNGNNGSGL 514  
QY 513 SLMPAYNLTEQYIQLDLNMSLGRLKEPRVDFWT 546  
DB 515 POMPAYDYKEGYLIQATTQAQKLDKEVAFWT 548

RESULT 7  
US-09-595-682B-26  
Sequence 26, Application US/09595682B  
Patent No. 6800483  
GENERAL INFORMATION:  
APPLICANT: Danks, Mary K.  
APPLICANT: Potter, Philip M.  
APPLICANT: Houghton, Peter J.  
TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of  
FILE REFERENCE: SJ-0005

CURRENT APPLICATION NUMBER: US/09/595,682B  
CURRENT FILING DATE: 2000-01-16  
PRIOR APPLICATION NUMBER: 60/075,258  
PRIOR FILING DATE: 1998-02-19  
PRIOR APPLICATION NUMBER: PCT/US99/03171  
PRIOR FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 26  
LENGTH: 543  
TYPE: PRT  
ORGANISM: Oryctolagus cuniculus  
US-09-595-682B-26

Query Match 36.7%; Score 1130.5; DB 4; Length 543;  
Best Local Similarity 43.7%; Pred. No. 3.5e-114;  
Matches 249; Conservative 75; Mismatches 179; Indels 67; Gaps 13;

QY 12 WCFELIQLPLGHRQMGKTPSABGFORNTLGMIOGKQVTVLGSPPVNVFLGVPFAAP 71  
DB 2 WLCALASLAACTAGH--PSAP--PVVDYVKGVLGKVFSLGFAQVAVFLGVPAKP 58  
QY 72 PLGSLRFTNPQAPSPMDNLRKATSYPNLCLNSEWLLDDQML-----KVHYP-KPGV 123  
DB 59 PLGSLRFAFPQAPAESHSVHKNTTSYPPWCSDA-----VSGHMLSELFTNRKENIPLKF-- 112  
QY 124 SEDCLYINLYAPAHADTSKLPVLVWFPFGAFKTPGASIFDGSALAAVEDLVVVOGYRL 183  
DB 113 SEDCLYINLYTPADLTKRGRLPVWVWVHGGGLMVGASTYDGLALSHENVVVTTIOYRL 172  
QY 184 GIGFETTTMDHAPQNMWAFKQOVAALSVQKNIFFPGDSSVTTFGESAGALSVSLL 243  
DB 173 GIGGFSTGDEHSRGNMCHLDQVAAALRWQDNINFGDPSYTFGESAGGSVSITLL 232  
QY 244 SPMAGLFHKAIMSGVAIIPYLEAHDYKSED--LQVVAHFCGNNADEBALLRCIRTK 301  
DB 233 SPLTKNLFHRAISSEGVALLSSL-----FRKNTSLAKIAIEAGCKTTTSAVWVHCLROK 288  
QY 302 PSKELL--TISQK-----TKSFTRVVDGAFPNNEBLDLSQKAFAPISITG 346  
DB 289 TEEELMEVTLKMKMALDVGDPRENTAFITTVIDGVLFPKAPAEILAEKKVMMLPYMG 348  
QY 347 VNNHECGFLPM-----KEAPEILSGNSKSLAHLIQLNIHIPPQYLAHA 392  
DB 349 INQOEFMIIIPMQLGYPLSEGLDKQKATLMLKS-----YPIVNSKELTPVAT 399  
QY 393 NEYHHDGSLTEIRDLSLDLIGVFFVVPALITARYHRDAGAVVYFYEPRHRPOCFEDTK 452  
DB 400 EKYIGCTDDPVKKKDLFLDMLADLLFGVPSVNVARHHRDAGAPTYVEYRVRPSSDMR 459  
QY 453 PAFVKADHADEVAFVFGAFLKGDIVMFEAGATEEELSRKMKKWATFARTGNNGNDL 512  
DB 460 PKTVIGDHGEIRSVLGAPFLK-----EGATEEELKLSKMKWAKWANFARNGNNGSGL 513  
QY 513 SLMPAYNLTEQYIQLDLNMSLGRLKEPRVDFWT 542  
DB 514 POMPAYDYKEGYLIQATTQAQKLDKEVAFWT 543

RESULT 8  
US-08-845-295A-2  
Sequence 2, Application US/08845295A  
Patent No. 5817490  
GENERAL INFORMATION:  
APPLICANT: Hubbs, John C.  
TITLE OF INVENTION: Enzymatic Process for the Manufacture of  
TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eastman Chemical Company  
STREET: P. O. Box 511  
CITY: Kingsport



STATE: Tennessee  
 COUNTRY: USA  
 ZIP: 37662-5075  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch disk  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows 95  
 SOFTWARE: Microsoft Word  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/845,295A  
 FILING DATE: 25-April-97  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/017,879  
 FILING DATE: 17-MAY-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cheryl J. Tubach  
 REGISTRATION NUMBER: 38,346  
 REFERENCE/DOCKET NUMBER: 70432  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 423-229-6189  
 TELEFAX: 423-229-1239  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 584 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 MOLECULE TYPE: protein  
 US-08-845-295A-2

Query Match 35.4%; Score 1091.5; DB 2; Length 584;  
 Best Local Similarity 43.8%; Pred. No. 7.4e-110;  
 Matches 259; Conservative 63; Mismatches 191; Indels 79; Gaps 17;

12 WCFLLDPLGLHROMGKTGPSAEGPQNTRLGWIQKQVTV--LGSPVPVNVFLGVPPA 69  
 2 WLLPVLTLSSASSATW--AGOPASPPVVDVTAQGRVLGKTVSLEGIAFTQPVAVFLGVPPA 59  
 70 APPLSLRFTNPQAPSPMDNLEATSYPNLCLONS--EMLLD-----QHMLKVHYPK 120  
 60 KPLSLSLRFPAPQAPSPMDNLEATSYPNLCLONS--EMLLD-----QHMLKVHYPK 117  
 121 FGVSEDCLYLNIYAPADADTSGKLPVLVWPGGAFKTSASIFDGSALAAYED--VLVVV 178  
 118 ---SEDCLYLNIYTPADLTGKGRLPVWVWIHGGGLVLGAPMYDGVVLAHNFVVVVA 174  
 179 VOYRLGIGFPTTWOAHAGNNAFKDOVAALSMVQKNIFFGSGDSVITIGES--AGAI 236  
 175 IQYRLGIGFPTTWOAHAGNNAFKDOVAALSMVQKNIFFGSGDSVITIGES--AGAI 234  
 237 SVSLSLSPMAKGLPHKAIMESGVALIPLYLEAHDYKESDLOVVAHFCGNNADESALLR 296  
 235 SVSLSLSPMAKGLPHKAIMESGVALIPLYLEAHDYKESDLOVVAHFCGNNADESALLR 294  
 235 SVSLSLSPMAKGLPHKAIMESGVALIPLYLEAHDYKESDLOVVAHFCGNNADESALLR 294  
 297 CLRTKPSKELLTLISOKTSGFT-----RVVDGAFPPNEPLDLISOK--AFK 339  
 295 CLRTKPSKELLTLISOKTSGFT-----RVVDGAFPPNEPLDLISOK--AFK 339  
 295 CLRTKPSKELLTLISOKTSGFT-----RVVDGAFPPNEPLDLISOK--AFK 339  
 295 CLRTKPSKELLTLISOKTSGFT-----RVVDGAFPPNEPLDLISOK--AFK 339  
 340 ALPSIIIGVNNHSGFLP-----MKAEPEILSGSNKSLALHILIONILAIIPQ 386  
 355 TVPYIYIGIKQEGHMLPTMGFPLSEGLDKQATSLMKS-----YPIANI-----DE 404  
 387 YHLLVANEFFHDKH-----SLTEIRSLDLGADVFPVVPALITAYHNDAGAPVYFYEF 441  
 405 ELTPVAT--FTDKYLGIGTDDPVKKKDLFLDLMGDDVFGVSVYVAQHNDAGAPVYFYEF 462  
 442 RHRPQCFED--TTPAVKADHADEVAFVFGAFLKSDIWMFEGATEEELSLSRKMKKYA 499  
 463 QYRPSRSSDKFTYKPVIVIGDHDEIFSVGFPILKDD-----APEEELSLSLTKVWKPFA 516  
 500 TPARTNPNNGNDLSLWP--AYNLTEOYLQJLDLMSIGORLKEBRVDFTWSTI 549  
 517 NFARSGNPNNGNDLSLWP--AYNLTEOYLQJLDLMSIGORLKEBRVDFTWSTI 568

RESULT 9  
 US-09-140-933-2  
 Sequence 2, Application US/09140933  
 Patent No. 6022719

GENERAL INFORMATION:  
 APPLICANT: Hubbs, John C.  
 TITLE OF INVENTION: Enzymatic Process for the Manufacture of  
 TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of  
 TITLE OF INVENTION: 2-Keto-L-Gulonic Acid  
 NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSES: Eastman Chemical Company  
 STREET: P. O. Box 511  
 CITY: Kingsport  
 STATE: Tennessee

COUNTRY: USA  
 ZIP: 37662-5075  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch disk  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows 95  
 SOFTWARE: Microsoft Word  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/140,933  
 FILING DATE: 27-August-98  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/017,879; 08/845,295  
 FILING DATE: 17-May-96; 25-April-97  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cheryl J. Tubach  
 REGISTRATION NUMBER: 38,346  
 REFERENCE/DOCKET NUMBER: 70432  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 423-229-6189  
 TELEFAX: 423-229-1239  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 584 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 MOLECULE TYPE: protein  
 US-09-140-933-2

Query Match 35.4%; Score 1091.5; DB 3; Length 584;  
 Best Local Similarity 43.8%; Pred. No. 7.4e-110;  
 Matches 259; Conservative 63; Mismatches 191; Indels 79; Gaps 17;

12 WCFLLDPLGLHROMGKTGPSAEGPQNTRLGWIQKQVTV--LGSPVPVNVFLGVPPA 69  
 2 WLLPVLTLSSASSATW--AGOPASPPVVDVTAQGRVLGKTVSLEGIAFTQPVAVFLGVPPA 59  
 70 APPLSLRFTNPQAPSPMDNLEATSYPNLCLONS--EMLLD-----QHMLKVHYPK 120  
 60 KPLSLSLRFPAPQAPSPMDNLEATSYPNLCLONS--EMLLD-----QHMLKVHYPK 117  
 121 FGVSEDCLYLNIYAPADADTSGKLPVLVWPGGAFKTSASIFDGSALAAYED--VLVVV 178  
 118 ---SEDCLYLNIYTPADLTGKGRLPVWVWIHGGGLVLGAPMYDGVVLAHNFVVVVA 174  
 179 VOYRLGIGFPTTWOAHAGNNAFKDOVAALSMVQKNIFFGSGDSVITIGES--AGAI 236  
 175 IQYRLGIGFPTTWOAHAGNNAFKDOVAALSMVQKNIFFGSGDSVITIGES--AGAI 234  
 237 SVSLSLSPMAKGLPHKAIMESGVALIPLYLEAHDYKESDLOVVAHFCGNNADESALLR 296  
 235 SVSLSLSPMAKGLPHKAIMESGVALIPLYLEAHDYKESDLOVVAHFCGNNADESALLR 294  
 297 CLRTKPSKELLTLISOKTSGFT-----RVVDGAFPPNEPLDLISOK--AFK 339  
 295 CLRTKPSKELLTLISOKTSGFT-----RVVDGAFPPNEPLDLISOK--AFK 339  
 295 CLRTKPSKELLTLISOKTSGFT-----RVVDGAFPPNEPLDLISOK--AFK 339  
 295 CLRTKPSKELLTLISOKTSGFT-----RVVDGAFPPNEPLDLISOK--AFK 339

QY 340 AIPSTIGVNNHCGFLLP-----MKEAPEILSGSNKSLALHLIIONLHIPPQ 386  
DB 355 TVPIYIVGINKOEFQMLPTWVGFPPLSGKLDQKTATSLMK-----YPIANI-----PE 404  
QY 387 YHLVANEYFHDKH-----SLTEIRDSLDDLGDFVFPVPAITARYHRDAGAPVYEF 441  
DB 405 ELTPVAT--FTDKYLGSTDDPVKKKDLFLDMGDVVFVGVSVTAHQHRDAGAPVYEF 462  
QY 442 RHRPOCFED--TKPAFYADHADEVRFVFGAFLKGDIVMEGATEEKLRSKMKYWA 499  
DB 463 QYRPSFSSDKFTKPKTYIGDHGEIPIVFGFPLKGD-----APEEVSLSKTYMKFWA 516  
QY 500 TPARTGNPNNDLSLP--AYNLTEOYLQDLNMSLGORLKEPRVDWTSTI 549  
DB 517 NFARSGPNGBGLPHWPFMTYDQEBGYLQIGVNTQAARKLKGEEVAFWNDDL 568

RESULT 10  
US-09-146-661-2  
Sequence 2, Application US/09146661  
Patent No. 6136575  
GENERAL INFORMATION:  
APPLICANT: Hubbs, John C.  
TITLE OF INVENTION: Enzymatic Process for the Manufacture of  
TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of 2-Keto-L-Gu-  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eastman Chemical Company  
STREET: P.O. Box 511  
CITY: Kingsport  
STATE: Tennessee  
COUNTRY: USA  
ZIP: 37662-5075  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/146,661  
FILING DATE: 03-September-98  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/017,879; 08/845,295  
FILING DATE: 17-May-96; 25-April-97  
ATTORNEY/AGENT INFORMATION:  
NAME: Cheryl J. Tubach  
REGISTRATION NUMBER: 38,346  
REFERENCE/DOCKET NUMBER: 70432  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 423-229-6189  
TELEFAX: 423-229-1239  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 584 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
MOLECULE TYPE: protein  
US-09-146-661-2

Query Match 35.4%; Score 1091.5; DB 3; Length 584;  
Best Local Similarity 43.8%; Pred. No. 7,4e-110;  
Matches 259; Conservative 63; Mismatches 191; Indels 79; Gaps 17;  
QY 12 WCFEFLIQLDHRQWGTGPAEGFORTRLGWIQKQVY--LGSVPVAVFLGVFA 69  
DB 2 WLLPLVLTLSASATW--AGQPASPPVVDYTAGRGVLGKTVSLEGLAFTQPAVFLGVFA 59  
QY 70 APPLSGLRPTNQPSPMNDLREATSYNCLIONS--EMLLD-----QHMLKVIYPK 120  
DB 60 KPPLGSLRPAPOAPAPWSPVKNITTSYPMCCQDPVVEQWMSDLFTNFTGKERLTLEF-- 117

QY 121 FGVEDCLYINITYAPAHADTGSKLPLYVMPFGGAFKTSASIRDSALAYED--VLVVV 178  
DB 118 ---SEDCYINITYPALTRGRRLPVWVTHGGGLVLGGAPMDGVVLAHENFTVVVVA 174  
QY 179 VQYRLGTFGFTTWDQAPGNWMAFKQVVALSWQKNIFFGGDPSSVTYIFGES--AGAI 236  
DB 175 IQYRLGTFGFTTWDQAPGNWMAFKQVVALSWQKNIFFGGDPSSVTYIFGES--AGAI 234  
QY 237 SVSLSLSPAKGLFKHAKMESGVALIPLYLEANDYKESDLOVVAHFQNNASDEALIR 296  
DB 235 SVSVLVISPLAKLFLRAISSEGVALTVALVRKDMQAARQIAVLACCTTYSAVFTVH 294  
QY 297 CLRTKSKELTLTISQTKSFT-----RVVDGAFAPNEPDLDSQK--AFK 339  
DB 295 CLRQKSEDELDDLTLMCKELTLDPHQDQESHPLPVTVDGVLLPKMEELIAEDPTFN 354  
QY 340 AIPSTIGVNNHCGFLLP-----MKEAPEILSGSNKSLALHLIIONLHIPPQ 386  
DB 355 TVPIYIVGINKOEFQMLPTWVGFPPLSGKLDQKTATSLMK-----YPIANI-----PE 404  
QY 387 YHLVANEYFHDKH-----SLTEIRDSLDDLGDFVFPVPAITARYHRDAGAPVYEF 441  
DB 405 ELTPVAT--FTDKYLGSTDDPVKKKDLFLDMGDVVFVGVSVTAHQHRDAGAPVYEF 462  
QY 442 RHRPOCFED--TKPAFYADHADEVRFVFGAFLKGDIVMEGATEEKLRSKMKYWA 499  
DB 463 QYRPSFSSDKFTKPKTYIGDHGEIPIVFGFPLKGD-----APEEVSLSKTYMKFWA 516  
QY 500 TPARTGNPNNDLSLP--AYNLTEOYLQDLNMSLGORLKEPRVDWTSTI 549  
DB 517 NFARSGPNGBGLPHWPFMTYDQEBGYLQIGVNTQAARKLKGEEVAFWNDDL 568

RESULT 11  
US-09-150-515-2  
Sequence 2, Application US/09150515  
Patent No. 6271006  
GENERAL INFORMATION:  
APPLICANT: Hubbs, John C.  
TITLE OF INVENTION: Enzymatic Process for the Manufacture of  
TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eastman Chemical Company  
STREET: P.O. Box 511  
CITY: Kingsport  
STATE: Tennessee  
COUNTRY: USA  
ZIP: 37662-5075  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/150,515  
FILING DATE: 09-SEP-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/017,879; 08/845,295  
FILING DATE: 17-May-96; 25-April-97  
ATTORNEY/AGENT INFORMATION:  
NAME: Cheryl J. Tubach  
REGISTRATION NUMBER: 38,346  
REFERENCE/DOCKET NUMBER: 70432  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 423-229-6189  
TELEFAX: 423-229-1239  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 584 amino acids



QY 125 EDCLYNTIYAPAHADTQSKLPVLWPFEGAFKPGSASIPGSGALAYEDVLVYVYQYRIG 18  
 Db 1 ECHLYNTIYTPADLPDKKRLPVMVWVHGGGLMGAASTYDGLALAAHEVYVYVYIYQYRIG 60  
 QY 185 IFGFPTMDQAHPGWMAFKDOVALLSWYQXIEFPFGDPSVYTIFGESGASIVSSYILS 244  
 Db 61 IGFSTGDSEHSRGWGHLDQVALRWYDNIASFNGNGSVYTI FGESAGESIVSYLVLS 120  
 QY 245 PMAKLPHKAIMESGVAIIPYLEAHDEYK--SEDLGVVNHFGCNGNASSSEKLLCLRTKP 302  
 Db 121 PLAKLPHRAAISGVALSYLVYKKGDVYPLAEQIYITL--GCKTYSAMWYCIROKT 177  
 QY 303 SKELLTTSQK-----TKSTFRVVDGAFFPNEBLDLSQKAFKAPISIIYV 347  
 Db 178 EEBLETTTLKIGNSYMTYRETQRESETLTGVIYDGLMLTKTPEELQGBERNHYPYVWGI 237  
 QY 348 NNHECGELLPMEKAPETLSGS--NKSLALHLQN---ILHLPQYHLVANEYFHDHGL 402  
 Db 238 NKQFEGWLIPMOQMSYPLBSGQLDQKTNASLSLGSPIPLFALAKLIPBATEKYLIGTDDT 297  
 QY 403 TELRDSLLDLGCVFVVVPLSITARYHRDAGAPVYFYEFRHRPOCFEDTGPATKADHD 462  
 Db 298 VKKDLIDLIDLAVWVGPSVIVANHRDAGAPTYMEFQYRPSFSMDMKPKYVIDHBD 357  
 QY 463 EVAFVEFGAFKLDKDIVMFGATGEEKLSRKQMKYATTFARTGNPBGNDLSIMPAYNLTLE 522  
 Db 358 ELRPSVFGAFPLK-----EGASEEITRISRKVMKFMANFARNGNPNGKGLPHMPEYNGE 411  
 QY 523 QYIQLDINNSLQURLKEPRVDFMTS 547  
 Db 412 GYIQLGANTQAOKLCKDEKVAFFWN 436

RESULT 14  
US-08-446-100-28  
Sequence 28, Application US/08446100  
Patent No. 6001625  
GENERAL INFORMATION:  
APPLICANT: Broomfield, Clarence A  
APPLICANT: Millard, Charles B  
APPLICANT: Lockridge, Oksana  
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hendricks and Assoc.  
STREET: 9669 A Main Street, P.O. Box 2509  
CITY: Fairfax  
STATE: VA  
COUNTRY: US  
ZIP: 22031  
COMPUTER READABLE FORM:

US-08-446-100-28

[illegible]

RESULT 15  
US-08-446-100-30  
; Sequence 30, Application US/08446100  
; Patent No. 6001625  
; GENERAL INFORMATION:  
; APPLICANT: Broomfield, Clarence A  
; APPLICANT: Millard, Charles B

Db 412 GYLOIGANTQAOKLKKOEVAFWTN 436  
Search completed: June 16, 2005, 20:46:37  
Job time : 46 secs

APPLICANT: Lockridge, Oksana  
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hendricks and Assoc.  
STREET: 9669 A Main Street, P.O. Box 2509  
CITY: Fairfax  
STATE: VA  
COUNTRY: US  
ZIP: 22031  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,100  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hendricks, Glenna  
REGISTRATION NUMBER: 32,535  
REFERENCE/DOCKET NUMBER: broomfield  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 425-4250  
TELEFAX: (703) 425-2767  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 454 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ANTI-SENSE: YES  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: human esterases  
US-08-446-100-30

Query Match 30.6%; Score 942.5; DB 3; Length 454;  
Best Local Similarity 44.9%; Pred. No. 9,5e-94;  
Matches 200; Conservative 64; Mismatches 150; Indels 31; Gaps 6;

QY 125 EDCLNTYAPAHADTGSKPLVWVFGAFKTSIFDGSALAEDEVLVVVVQYRLG 184  
DB 1 EHCLNTYITPADLTKKRLPVMVHGGGLMVGASTYDGLAAHENVVVTIQYRLG 60  
QY 185 IFGFPTTDHAPGNMAFQDQVAALSWQKNIFFGDPSSVTIFGESAGAISVSLLS 244  
DB 61 IWFSTGDEHSGRGWGHLDQVAALRWQDNASFGNPGSVTIFGESAGSESVALVLS 120  
QY 245 PMAKGLFHAKMESGVALIIPYLEAHDYEK--SEDLQVVAHFGNNASDSEALLRCLRTKP 302  
DB 121 PLAKNLFHRAISESGVALSVLVKKGDVPLAEQIAITA--GCKTTTSAAMVHCLROKT 177  
QY 303 SKELLTLSGK-----TKSFTRVVDGAFPNBPLDLLSOKAFKAPISIIIGV 347  
DB 178 EEELETTLKIGNSTVLTMYRQTHSTLIGTVIDGMLIKTPEELQRENFHTVPMWGI 237  
QY 348 NNHECGFLPMKEAPEILSGS--NKSLLAHLIQN--ILHIPPQYLHLVANEYFHDKSL 402  
DB 238 NKQEGFWLIPQMLSVPLSEGQLDQKTMSLSGSPIPLFAIKELIPBATEKYLGTDT 297  
QY 403 TEIRDSLDDLCDVFPVVPALITATYHRDAGAPVTFYEFRRHPQCEPDTKPAFVKADHAD 462  
DB 238 VKKKDLIIDLIDVWFGVPSVIVANHRDAGAPTYWYEPQYRPSFSSDMKPKTVIGDHG 357  
QY 463 EYRFVFGGAFLEKGDVMEFGATEEELLSRKKMKWATFARQNGNDLSLMPAYNLTE 522  
DB 358 ELFSVFGAPFLK-----EGASEEETIRUSKMKFANFARNGNPVKGCLPHMPEYNQKE 411  
QY 523 QYLOLDLNNSLGQRLKEPRVDPMTS 547



GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: June 16, 2005, 20:45:08 ; Search time 158 Seconds  
(without alignments)  
1411.975 Million cell updates/sec

Title: US-10-674-636-2

Perfect score: 3079  
Sequence: 1 MPOGUTSSASQWCFLLIQP.....PLSLITFLSLIQPFPPFCAP 581

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCF\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
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5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
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12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US10F\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep:\*  
20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3079	100.0	581	13	US-10-023-515-2	Sequence 2, Appli
2	3079	100.0	581	15	US-10-674-636-2	Sequence 2, Appli
3	3079	100.0	581	16	US-10-757-262-46	Sequence 46, Appli
4	2915	99.7	575	15	US-10-451-168-91	Sequence 91, Appli
5	2900	99.2	642	15	US-10-433-256-10	Sequence 10, Appli
6	2607.5	84.7	581	15	US-10-451-168-92	Sequence 92, Appli
7	2506	84.6	525	15	US-10-094-749-2375	Sequence 2375, Ap
8	2597.5	84.1	581	15	US-10-114-270-196	Sequence 196, App
9	2588.5	84.1	618	15	US-10-381-898-2	Sequence 2, Appli
10	2454	79.7	469	15	US-10-104-047-2219	Sequence 2219, Ap
11	1985	64.5	542	16	US-10-233-933A-2	Sequence 2, Appli

12	1985	64.5	542	16	US-10-233-933A-2	Sequence 4, Appli
13	1780	57.8	356	15	US-10-451-168-93	Sequence 93, Appli
14	1230	39.9	549	9	US-09-925-298-689	Sequence 689, App
15	1230	39.9	550	14	US-10-102-806-689	Sequence 689, App
16	1230	39.9	549	15	US-10-267-756-5	Sequence 5, Appli
17	1230	39.9	559	16	US-10-858-271-28	Sequence 28, Appli
18	1186.5	38.5	554	9	US-09-895-860-4	Sequence 4, Appli
19	1186.5	38.5	554	15	US-10-377-072-4	Sequence 4, Appli
20	1186.5	38.5	554	16	US-10-377-072-4	Sequence 4, Appli
21	1179.5	38.3	571	11	US-09-911-836-23	Sequence 23, Appli
22	1179.5	38.3	571	11	US-09-833-245-1090	Sequence 1090, Ap
23	1179.5	38.3	571	13	US-10-036-342-23	Sequence 23, Appli
24	1179.5	38.3	571	13	US-10-036-041-23	Sequence 23, Appli
25	1179.5	38.3	571	14	US-10-028-072-542	Sequence 542, App
26	1179.5	38.3	571	14	US-10-035-855-23	Sequence 23, Appli
27	1179.5	38.3	571	14	US-10-140-808-542	Sequence 542, App
28	1179.5	38.3	571	14	US-10-121-049-542	Sequence 542, App
29	1179.5	38.3	571	14	US-10-123-804-542	Sequence 542, App
30	1179.5	38.3	571	14	US-10-140-808-542	Sequence 542, App
31	1179.5	38.3	571	14	US-10-175-746-542	Sequence 542, App
32	1179.5	38.3	571	14	US-10-176-918-542	Sequence 542, App
33	1179.5	38.3	571	14	US-10-176-921-542	Sequence 542, App
34	1179.5	38.3	571	14	US-10-227-884-210	Sequence 210, App
35	1179.5	38.3	571	14	US-10-036-214-23	Sequence 23, Appli
36	1179.5	38.3	571	14	US-10-137-865-542	Sequence 542, App
37	1179.5	38.3	571	14	US-10-140-808-542	Sequence 542, App
38	1179.5	38.3	571	14	US-10-035-719-23	Sequence 23, Appli
39	1179.5	38.3	571	14	US-10-142-431-542	Sequence 542, App
40	1179.5	38.3	571	14	US-10-143-114-542	Sequence 542, App
41	1179.5	38.3	571	14	US-10-230-163-210	Sequence 210, App
42	1179.5	38.3	571	14	US-10-036-160-23	Sequence 23, Appli
43	1179.5	38.3	571	14	US-10-230-338-210	Sequence 210, App
44	1179.5	38.3	571	14	US-10-142-419-542	Sequence 542, App
45	1179.5	38.3	571	14	US-10-218-631-210	Sequence 210, App

ALIGNMENTS

RESULT 1  
US-10-023-515-2  
Sequence 2, Application US/10023515  
Publication No. US20020182636A1  
GENERAL INFORMATION:  
APPLICANT: Sinos-Santiago, Immaculada  
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYESTERASE  
FILE REFERENCE: 10448-122001  
CURRENT FILING DATE: 2001-12-18  
PRIOR FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: 60/256,369  
PRIOR FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: 60/279,508  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 581  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-023-515-2

Query Match	100.0%	Score 3079;	DB 13;	Length 581;
Beet Local Similarity	100.0%	Pred. No. 1.1e-277;	Indels	0;
Matches	581;	Conservative	0;	Gaps 0;
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DB	1	MPOGUTSSASQWCFLLIQPILGHRQMGKTPSAEGPQNRRLGWIQCKQVTVLGSPPV	60	
QY	61	NVFLGVPAAAPLGLRFTNPQAPSPWDNLRDATSYPLCLQNSEWILLDDHMLKHYPK	120	

Db 61 NVFLGVPFAAPPLSLFTNPOPASPWDNIREATSYENLCLQNSEWILLDQHLKATYHPK 120  
QY 121 FGVEDCLYINITYAPAHADTGSKLPLVWMPGGAFTGASIFDGSALAYEDVLVWVQ 180  
Db 121 FGVEDCLYINITYAPAHADTGSKLPLVWMPGGAFTGASIFDGSALAYEDVLVWVQ 180  
QY 181 YRLGI FGFEFTTMOHAPGNNAFKDQVVALSWQKNIEFGGDPSSVTTFGESAGAISSVS 240  
Db 181 YRLGI FGFEFTTMOHAPGNNAFKDQVVALSWQKNIEFGGDPSSVTTFGESAGAISSVS 240  
QY 241 LILSPMAKGLFHKAINESGVAIIPYLEADHYEKSEDLQVVAFFCGNNSDSALLRCURT 300  
Db 241 LILSPMAKGLFHKAINESGVAIIPYLEADHYEKSEDLQVVAFFCGNNSDSALLRCURT 300  
QY 301 KPSKELLTTSOKTKSTFRVVDGAFPPNEBPLDLSQKAFKAIPIIIGVNNHECGFLLPKE 360  
Db 301 KPSKELLTTSOKTKSTFRVVDGAFPPNEBPLDLSQKAFKAIPIIIGVNNHECGFLLPKE 360  
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Db 361 APEILSGNKSJLALHILQNIILHIPOYLHLVANEYFHDHSLTEIRDSLLDLGDVFFV 420  
QY 421 PALITARYRDAGAPVYFEFFRHPQCFEDTKPAFVKADHAEVAFVFGAFLKGDIVMF 480  
Db 421 PALITARYRDAGAPVYFEFFRHPQCFEDTKPAFVKADHAEVAFVFGAFLKGDIVMF 480  
QY 481 EGATEEKLISRQMKKYATFARTGNPNDLSLMPAYNLTEOYLQDLNWSLQRLKEP 540  
Db 481 EGATEEKLISRQMKKYATFARTGNPNDLSLMPAYNLTEOYLQDLNWSLQRLKEP 540  
QY 541 RVDFTWSTIPLILSASDMLHSPSLSTFLSLQPFEEFCAP 581  
Db 541 RVDFTWSTIPLILSASDMLHSPSLSTFLSLQPFEEFCAP 581

RESULT 2  
US-10-674-636-2  
; Sequence 2, Application US/10674636  
; Publication No. US20040086922A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rofy A. J.  
; APPLICANT: Silos-Santiago, Immaculada  
; TITLE OF INVENTION: 5310, A NOVEL HUMAN CARBOXYLSTERASE  
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF  
; FILE REFERENCE: 10448-12201  
; CURRENT APPLICATION NUMBER: US/10/674,636  
; PRIOR FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: US/10/023,515  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: 60/256,369  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: 60/279,508  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 581  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-674-636-2

Query Match 100.0%; Score 3079; DB 15; Length 581;  
Best Local Similarity 100.0%; Pred. No. 1,1e-277;  
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEOGLTSSASQWCFPLIIOPLLGHROWGKTGSPAGSPORNTRLGWIQGOYVIGSPVPV 60  
Db 1 MEOGLTSSASQWCFPLIIOPLLGHROWGKTGSPAGSPORNTRLGWIQGOYVIGSPVPV 60  
QY 61 NVFLGVPFAAPPLSLFTNPOPASPWDNIREATSYENLCLQNSEWILLDQHLKATYHPK 120  
Db 61 NVFLGVPFAAPPLSLFTNPOPASPWDNIREATSYENLCLQNSEWILLDQHLKATYHPK 120

QY 121 FGVEDCLYINITYAPAHADTGSKLPLVWMPGGAFTGASIFDGSALAYEDVLVWVQ 180  
Db 121 FGVEDCLYINITYAPAHADTGSKLPLVWMPGGAFTGASIFDGSALAYEDVLVWVQ 180  
QY 181 YRLGI FGFEFTTMOHAPGNNAFKDQVVALSWQKNIEFGGDPSSVTTFGESAGAISSVS 240  
Db 181 YRLGI FGFEFTTMOHAPGNNAFKDQVVALSWQKNIEFGGDPSSVTTFGESAGAISSVS 240  
QY 241 LILSPMAKGLFHKAINESGVAIIPYLEADHYEKSEDLQVVAFFCGNNSDSALLRCURT 300  
Db 241 LILSPMAKGLFHKAINESGVAIIPYLEADHYEKSEDLQVVAFFCGNNSDSALLRCURT 300  
QY 301 KPSKELLTTSOKTKSTFRVVDGAFPPNEBPLDLSQKAFKAIPIIIGVNNHECGFLLPKE 360  
Db 301 KPSKELLTTSOKTKSTFRVVDGAFPPNEBPLDLSQKAFKAIPIIIGVNNHECGFLLPKE 360  
QY 361 APEILSGNKSJLALHILQNIILHIPOYLHLVANEYFHDHSLTEIRDSLLDLGDVFFV 420  
Db 361 APEILSGNKSJLALHILQNIILHIPOYLHLVANEYFHDHSLTEIRDSLLDLGDVFFV 420  
QY 421 PALITARYRDAGAPVYFEFFRHPQCFEDTKPAFVKADHAEVAFVFGAFLKGDIVMF 480  
Db 421 PALITARYRDAGAPVYFEFFRHPQCFEDTKPAFVKADHAEVAFVFGAFLKGDIVMF 480  
QY 481 EGATEEKLISRQMKKYATFARTGNPNDLSLMPAYNLTEOYLQDLNWSLQRLKEP 540  
Db 481 EGATEEKLISRQMKKYATFARTGNPNDLSLMPAYNLTEOYLQDLNWSLQRLKEP 540  
QY 541 RVDFTWSTIPLILSASDMLHSPSLSTFLSLQPFEEFCAP 581  
Db 541 RVDFTWSTIPLILSASDMLHSPSLSTFLSLQPFEEFCAP 581

RESULT 3  
US-10-757-262-46  
; Sequence 46, Application US/10757262  
; Publication No. US20040197825A1  
; GENERAL INFORMATION:  
; APPLICANT: Karichevi, Venkateswarlu  
; APPLICANT: Eliasof, Scott D.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,  
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,  
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43229, 44373, 5164,  
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,  
; TITLE OF INVENTION: 18547, 115, 579, 15985, 18625, 760, 18603, 2395, 2554, 8675,  
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,  
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 2165, 30911, 41897, 1643,  
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR  
; FILE REFERENCE: MPIO3-007PILNOMNIM  
; CURRENT APPLICATION NUMBER: US/10/757,262  
; PRIOR FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 60/440,318  
; PRIOR FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: US 60/444,783  
; PRIOR FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: US 60/457,901  
; PRIOR FILING DATE: 2003-03-27  
; PRIOR APPLICATION NUMBER: US 60/468,775  
; PRIOR FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: US 60/471,614  
; PRIOR FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: US 60/478,742  
; PRIOR FILING DATE: 2003-06-16  
; PRIOR APPLICATION NUMBER: US 60/488,529  
; PRIOR FILING DATE: 2003-07-18  
; PRIOR APPLICATION NUMBER: US 60/491,156  
; PRIOR FILING DATE: 2003-07-30  
; PRIOR APPLICATION NUMBER: US 60/499,594  
; PRIOR FILING DATE: 2003-09-02  
; PRIOR APPLICATION NUMBER: US 60/506,332



;; PRIOR FILING DATE: 2003-09-26  
 ;; NUMBER OF SEQ ID NOS: 136  
 ;; SOFTWARE: FastSeq for Windows Version 4.0  
 ;; SEQ ID NO 46  
 ;; LENGTH: 581  
 ;; TYPE: PRT  
 ;; ORGANISM: Homo sapiens  
 US-10-757-262-46

Query Match 100.0%; Score 3079; DB 16; Length 581;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-277; Indels 0; Gaps 0;  
 Matches 581; Conservative 0; Mismatches 0;

Qy 1 MPOGLTSSASQWCFELIQLPLIGHROMKGTSPSAEGPQNRRLGNIQKQVTVLGSPPV 60  
 Db 1 MPOGLTSSASQWCFELIQLPLIGHROMKGTSPSAEGPQNRRLGNIQKQVTVLGSPPV 60  
 Qy 61 NVFLGVPPAAPPLGSLRFTNPQSPASPMNDLRBATSYPNLCLQNSMILLDQMLKVHYPK 120  
 Db 61 NVFLGVPPAAPPLGSLRFTNPQSPASPMNDLRBATSYPNLCLQNSMILLDQMLKVHYPK 120  
 Qy 121 FGVEDDCYLNIYAPAHADTGSKLPLYVWFGAFKTSASIFDGSALAAVEDVLVWVQ 180  
 Db 121 FGVEDDCYLNIYAPAHADTGSKLPLYVWFGAFKTSASIFDGSALAAVEDVLVWVQ 180  
 Qy 181 YRLGIFGFTTWDQHPGNMAFKDQVAAALSWQKNIIEFGDPSSVTIFGESAGAI SVSS 240  
 Db 181 YRLGIFGFTTWDQHPGNMAFKDQVAAALSWQKNIIEFGDPSSVTIFGESAGAI SVSS 240  
 Qy 241 LIISPMAGLFRHAKIMESGVAIIPYLEAHDYKESDLOVVAHFCGNNASDSEALIRCLRT 300  
 Db 241 LIISPMAGLFRHAKIMESGVAIIPYLEAHDYKESDLOVVAHFCGNNASDSEALIRCLRT 300  
 Qy 301 KPSKELLTQKTSFTFVNDGAFPPNEPLDLSQKAKAIPSIIGVNNHCGFLPMKE 360  
 Db 301 KPSKELLTQKTSFTFVNDGAFPPNEPLDLSQKAKAIPSIIGVNNHCGFLPMKE 360  
 Qy 361 APETLGSNKSALALHIONILHIIPQYLAHLVANEYFHDKSLTEIRDSLDDLGLGVFVV 420  
 Db 361 APETLGSNKSALALHIONILHIIPQYLAHLVANEYFHDKSLTEIRDSLDDLGLGVFVV 420  
 Qy 421 PALITARYHADGAVFYEFRRHRCQCFEDTKPAFKADHDEVAFVFGAFLKGDIVWF 480  
 Db 421 PALITARYHADGAVFYEFRRHRCQCFEDTKPAFKADHDEVAFVFGAFLKGDIVWF 480  
 Qy 481 EGATEEBEKLRSKMKYATPARTGNPNNDLSLMPAYNLTEQYQLDLNMSLGRLKEP 540  
 Db 481 EGATEEBEKLRSKMKYATPARTGNPNNDLSLMPAYNLTEQYQLDLNMSLGRLKEP 540  
 Qy 541 RVDFMTSTIPLILSASDMLHSPLSLTLFSLLOPFFFCAP 581  
 Db 541 RVDFMTSTIPLILSASDMLHSPLSLTLFSLLOPFFFCAP 581

RESULT 4  
 US-10-451-168-91  
 ; Sequence 91, Application US/10451168  
 ; Publication No. US20040091969A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SMITHKLINE BEECHAM CORPORATION  
 ; APPLICANT: SMITHKLINE BEECHAM P.L.C.  
 ; APPLICANT: GLAXO GROUP LIMITED  
 ; TITLE OF INVENTION: NOVEL COMPOUNDS  
 ; FILE REFERENCE: GP50039  
 ; CURRENT APPLICATION NUMBER: US/10/451,168  
 ; CURRENT FILING DATE: 2003-11-12  
 ; PRIOR APPLICATION NUMBER: PCT/US01/49232  
 ; PRIOR FILING DATE: 2000-12-17  
 ; PRIOR APPLICATION NUMBER: 60/256,710  
 ; PRIOR FILING DATE: 2000-12-19  
 ; PRIOR APPLICATION NUMBER: 60/257,048  
 ; PRIOR FILING DATE: 2000-12-20  
 ; PRIOR APPLICATION NUMBER: 60/260,482

;; PRIOR FILING DATE: 2001-01-09  
 ;; PRIOR APPLICATION NUMBER: 60/264,922  
 ;; PRIOR FILING DATE: 2001-01-30  
 ;; PRIOR APPLICATION NUMBER: 60/266,797  
 ;; PRIOR FILING DATE: 2001-02-06  
 ;; PRIOR APPLICATION NUMBER: 60/276,988  
 ;; PRIOR FILING DATE: 2001-03-19  
 ;; PRIOR APPLICATION NUMBER: 60/281,535  
 ;; PRIOR FILING DATE: 2001-04-04  
 ;; PRIOR APPLICATION NUMBER: 60/289,622  
 ;; PRIOR FILING DATE: 2002-06-28  
 ;; NUMBER OF SEQ ID NOS: 110  
 ;; SOFTWARE: FastSeq for Windows Version 4.0  
 ;; SEQ ID NO 91  
 ;; LENGTH: 575  
 ;; TYPE: PRT  
 ;; ORGANISM: Homo sapiens  
 US-10-451-168-91

Query Match 94.7%; Score 2915; DB 15; Length 575;  
 Best Local Similarity 97.0%; Pred. No. 2,1e-262;  
 Matches 553; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

Qy 12 WCFPLIQLPLIGHROMKGTSPSAEGPQNRRLGNIQKQVTVLGSPPVNVFLGVFPAP 71  
 Db 14 WAIWVLAAP-----TKGPSAEGPQNRRLGNIQKQVTVLGSPPVNVFLGVFPAP 65  
 Qy 72 PLGSLRFTNPQSPASPMNDLRBATSYPNLCLQNSMILLDQMLKVHYPKFVSEDCLYLN 131  
 Db 66 PLGSLRFTNPQSPASPMNDLRBATSYPNLCLQNSMILLDQMLKVHYPKFVSEDCLYLN 125  
 Qy 132 IYAPAHADTGSKLPLYVWFGAFKTSASIFDGSALAAVEDVLVWVQYRLGIFGFTT 191  
 Db 126 IYAPAHADTGSKLPLYVWFGAFKTSASIFDGSALAAVEDVLVWVQYRLGIFGFTT 185  
 Qy 192 WDQHPGNMAFKDQVAAALSWQKNIIEFGDPSSVTIFGESAGAI SVSSILSPMAKGLF 251  
 Db 186 WDQHPGNMAFKDQVAAALSWQKNIIEFGDPSSVTIFGESAGAI SVSSILSPMAKGLF 245  
 Qy 252 HKAIMESGVAIIPYLEAHDYKESDLOVVAHFCGNNASDSEALIRCLRTKPSKELLTSLQ 311  
 Db 246 HKAIMESGVAIIPYLEAHDYKESDLOVVAHFCGNNASDSEALIRCLRTKPSKELLTSLQ 305  
 Qy 312 KTKSFTRVVDGAFPPNEPLDLSQKAKAIPSIIGVNNHCGFLPMKEAPEILSGSNKS 371  
 Db 306 KTKSFTRVVDGAFPPNEPLDLSQKAKAIPSIIGVNNHCGFLPMKEAPEILSGSNKS 365  
 Qy 372 LALHLIONILHIIPQYLAHLVANEYFHDKSLTEIRDSLDDLGLGVFVVFPALITARYRD 431  
 Db 366 LALHLIONILHIIPQYLAHLVANEYFHDKSLTEIRDSLDDLGLGVFVVFPALITARYRD 425  
 Qy 432 AGAPVYEFERHRCQCFEDTKPAFKADHDEVAFVFGAFLKGDIVWFEGATEEBEKL 491  
 Db 426 AGAPVYEFERHRCQCFEDTKPAFKADHDEVAFVFGAFLKGDIVWFEGATEEBEKL 485  
 Qy 492 RKMCKYATPARTGNPNNDLSLMPAYNLTEQYQLDLNMSLGRLKEPRVDFMTSTIPL 551  
 Db 486 RKMCKYATPARTGNPNNDLSLMPAYNLTEQYQLDLNMSLGRLKEPRVDFMTSTIPL 545  
 Qy 552 ILSASDMLHSPLSLTLFSLLOPFFFCAP 581  
 Db 546 ILSASDMLHSPLSLTLFSLLOPFFFCAP 575

RESULT 5  
 US-10-433-256-10  
 ; Sequence 10, Application US/10433256  
 ; Publication No. US20040081980A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SANJANWALA, Madhusudan M.; YAO, Monique G.  
 ; APPLICANT: AU-YOUNG, Janice K.; BAUGHN, Mariah R.  
 ; APPLICANT: ARVIZU, Chandra S.; RING, HuiJun Z.  
 ; APPLICANT: LEE, Ernestine A.; DING, Li

```
APPLICANT: HAPALIA, April J.A.; TANG, Y. Tom
APPLICANT: YUE, Henry; TRIBOULEY, Catherine M.
APPLICANT: LU, Dying Anna M.; LAL, Preeti G.
APPLICANT: WARREN, Bridget A.; YANG, Junming
APPLICANT: CHAMLA, Narinder K.; NGUYEN, Daniel B.
APPLICANT: GANDHI, Ameena R.; LU, Yan
APPLICANT: ISON, Craig H.
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
FILE REFERENCE: PI-0113 USN
CURRENT APPLICATION NUMBER: US/10/433,256
CURRENT FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: PCT/US01/47429
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 60/254,308
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US 60/256,189
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/257,713
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: US 60/262,706
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/266,020
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PERL Program
SEQ ID NO 10
LENGTH: 642
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 6538080CD1
US-10-433-256-10
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Query Match          94.2%; Score 2900; DB 15; Length 642;
Best Local Similarity 99.5%; Pred. No. 6.36-261;
Matches 548; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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Qy 31 GPSAEGPQNRRLGMIQKQVTVLGSPPVNVFLGVFPAAPPLGSGRFTNPOASPMNDL 90
Db 92 GPSAEGPQNRRLGMIQKQVTVLGSPPVNVFLGVFPAAPPLGSGRFTNPOASPMNDL 151
Qy 91 REATSYNPLCLQNSEWMLLDQHMLKVHYPRFGVSEDCLYNTPAHPADTGSRLPYLVWF 150
Db 152 REATSYNPLCLQNSEWMLLDQHMLKVHYPRFGVSEDCLYNTPAHPADTGSRLPYLVWF 211
Qy 151 PGCAFKTGSASIFDGSALAAVEDLVVVVQYRLGIGFFTTMOHAPGMAFPDQYVALS 210
Db 152 PGCAFKTGSASIFDGSALAAVEDLVVVVQYRLGIGFFTTMOHAPGMAFPDQYVALS 211
Qy 211 WQGNIEFFEGDPSVITIFGESAGAISVSLLISPAKGLFHKAIMESGVAIIPYLEAHD 270
Db 272 WQGNIEFFEGDPSVITIFGESAGAISVSLLISPAKGLFHKAIMESGVAIIPYLEAHD 331
Qy 271 YKSESDLOVVAHFCGNNASDEALRLCLRTKPSKELLTTSOKTKSTRVVDGAFPPNEPL 330
Db 332 YKSESDLOVVAHFCGNNASDEALRLCLRTKPSKELLTTSOKTKSTRVVDGAFPPNEPL 391
Qy 331 DLISQAFKAIPIISIGVNNHECGFLLPMKEAPEIISGNSKSLALHLIOMLIHIPOYALH 390
Db 392 DLISQAFKAIPIISIGVNNHECGFLLPMKEAPEIISGNSKSLALHLIOMLIHIPOYALH 451
Qy 391 VANEYFHDHGSLEIRDSLLDLGDFVFPVPLIARHYRDAGADVFEFRRHQCFED 450
Db 452 VANEYFHDHGSLEIRDSLLDLGDFVFPVPLIARHYRDAGADVFEFRRHQCFED 511
Qy 451 TKPAFAKADHADEVFVFGAFLKGDIVMFBGATEEELSLRKMKNWATARCPNPN 510
Db 512 TKPAFAKADHADEVFVFGAFLKGDIVMFBGATEEELSLRKMKNWATARCPNPN 571
Qy 511 DLSLWPAVLTQOYLQDLNNSLGQRKLEPRVDFTSTIPIILASDMLSHPLSLTFLS 570
Db 572 DLSLWPAVLTQOYLQDLNNSLGQRKLEPRVDFTSTIPIILASDMLSHPLSLTFLS 631
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Qy 571 LLOPFFFCAP 581
Db 632 LLOPFFFCAP 642
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```
RESULT 6
US-10-451-168-92
Sequence 92, Application US/10451168
Publication No. US20040091969A1
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/US01/49232
PRIOR FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 92
LENGTH: 581
TYPE: PRT
ORGANISM: Homo sapiens
US-10-451-168-92
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Query Match          84.7%; Score 2607.5; DB 15; Length 581;
Best Local Similarity 91.4%; Pred. No. 1e-233;
Matches 499; Conservative 7; Mismatches 25; Indels 15; Gaps 3;
```

```
Qy 12 WCFLLIQPLILGRQKCTGPSAEGPQNRRLGMIQKQVTVLGSPPVNVFLGVFPAAP 71
Db 14 WAIWVLAP-----TKGPSAEGPQNRRLGMIQKQVTVLGSPPVNVFLGVFPAAP 65
Qy 72 PLGSLRFTNPOASPMNDLREATSYNPLCLQNSEWMLLDQHMLKVHYPRFGVSEDCLYN 131
Db 66 PLGSLRFTNPOASPMNDLREATSYNPLCLQNSEWMLLDQHMLKVHYPRFGVSEDCLYN 125
Qy 132 IYAPAHDTGSKLPLYLVMPFGAFTGSASIFDGSALAAVEDLVVVVQYRLGIGFFTT 191
Db 126 IYAPAHDTGSKLPLYLVMPFGAFTGSASIFDGSALAAVEDLVVVVQYRLGIGFFTT 185
Qy 192 WQAHAPGNAFQKQYVALSWQGNIEFFEGDPSVITIFGESAGAISVSLLISPAKGLF 251
Db 186 WQAHAPGNAFQKQYVALSWQGNIEFFEGDPSVITIFGESAGAISVSLLISPAKGLF 245
Qy 252 HKAIMESGVAIIPYLEAHDYKSESDLOVVAHFCGNNASDEALRLCLRTKPSKELLTSLQ 311
Db 246 HKAIMESGVAIIPYLEAHDYKSESDLOVVAHFCGNNASDEALRLCLRTKPSKELLTSLQ 305
Qy 312 KTKSFTRVVDGAFPPNEPLDLISQAFKAIPIISIGVNNHECGFLLPMKE--APEILSGN 369
Db 306 KTKSFTRVVDGAFPPNEPLDLISQAFKAIPIISIGVNNHECGFLLPMWRILAAVHTATPSN 365
Qy 370 KSLAL-----HLIOMLIHIPOYALH VANEYFHDHGSLEIRDSLLDLGDFVFPVVALI 424
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Db 366 RDALASTAGHFRHQH1PPOYLH.VANNEYFHDGSLTEIRDSILDLDGDFVFPAL1 425  
Qy 425 TARVHRDGAIVYEFEEFRRPOCFEDTKPAPYKADHAEVRFVFGAFLKGDIVFBEAT 484  
Db 426 TARVHRDGAIVYEFEEFRRPOCFEDTKPAPYKADHAEVRFVFGAFLKGDIVFBEAT 485  
Qy 485 EEBKLSRKMKYATFARTGNPNDLSLWPAVNLTEOYLQDLNMSLGQRLKEPRVD 544  
Db 486 EEBKLSRKMKYATFARTGNPNDLSLWPAVNLTEOYLQDLNMSLGQRLKEPRVD 545  
Qy 545 WTSTP 550  
Db 546 WWTGP 551

## RESULT 7

US-10-094-749-2375  
Sequence 2375, Application US/10094749  
Publication No. US20030219741A1

## GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO  
APPLICANT: SUGIYAMA, TOMOYASU  
APPLICANT: OTSUKI, TETSUJI  
APPLICANT: WAKAMATSU, AI  
APPLICANT: SATO, HIROYUKI  
APPLICANT: ISHII, SHIZUKO  
APPLICANT: YAMAMOTO, JUN-ICHI  
APPLICANT: ISONO, YUUKO  
APPLICANT: HIO, YURI  
APPLICANT: OTSUKA, KAORU  
APPLICANT: NAGAI, KEIICHI  
APPLICANT: IRIE, RYOTARO  
APPLICANT: TAMECHIKA, ICHIRO  
APPLICANT: SEKI, NAOHKO  
APPLICANT: YOSHIKAWA, TSUTOMU  
APPLICANT: OTSUKA, MOTOMYUKI  
APPLICANT: NAGAHARI, KENJI  
APPLICANT: MASUHO, YASUHIKO  
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA  
FILE REFERENCE: 08435/0160  
CURRENT APPLICATION NUMBER: US/10/094,749  
CURRENT FILING DATE: 2002-03-12  
PRIOR APPLICATION NUMBER: 60/350,435  
PRIOR FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: JP 2001-328381  
NUMBER OF SEQ ID NOS: 3381  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 2375  
LENGTH: 525  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-094-749-2375

Query Match 84.6% Score 2606; DB 15; Length 525;

Best Local Similarity 90.9%; Pred. No. 1,2e-233;

Matches 501; Conservative 0; Mismatches 0; Indels 50; Gaps 1;

Qy 31 GPSAAGPQNRRLGWIQCKQVTVLGSPPVNVNVLGVPAAPLGLRFTNPQSPAWN 90  
Db 25 GPSAAGPQNRRLGWIQCKQVTVLGSPPVNVNVLGVPAAPLGLRFTNPQSPAWN 84  
Qy 91 REATSYPNLCLONSWMLLDQMLKVHPKFGVSDCLYNTIYAPAHADTSGKLPVLWF 150  
Db 85 REATSYPNLCLONSWMLLDQMLKVHPKFGVSDCLYNTIYAPAHADTSGKLPVLWF 144  
Qy 151 PGAKRTGSASIFDGSALAAVEDVWVVOYRLGIFGFTTMDQAPGNMAFKDQVAALS 210  
Db 145 PGAKRTGSASIFDGSALAAVEDVWVVOYRLGIFGFTTMDQAPGNMAFKDQVAALS 204  
Qy 211 WVKNIIEFGDPSSVTTFGESAGAIVSSLLSPMAKGLFHKAIMSGVALIIPYLEAH 270

Db 205 WVKNIIEFGDPSSVTTFGESAGAIVSSLLSPMAKGLFHKAIMSGVALIIPYLEAH 264  
Qy 271 YEKSEDLQVNAHFCGNNADEALLRCLRTKSPKELLTSQTKSFTRVNDGAFEPNEPL 330  
Db 265 YEKSEDLQVNAHFCGNNADEALLRCLRTKSPKELLTSQTKSFTRVNDGAFEPNEPL 324  
Qy 331 DLSQKAFKAIPSIIGVNNHECGFLPMKEAPEILSGSNLSALHLIONIIHIPQYLHL 390  
Db 325 DLSQKAFKAIPSIIGVNNHECGFLPMKEAPEILSGSNLSALHLIONIIHIPQYLHL 384  
Qy 391 VANEYFHDKSLTTRISLDLDLDGVEFVVPALITARYHRACAPVYFEERHRPOCED 450  
Db 385 VANEYFHDKSLTTRISLDLDLDGVEFVVPALITARYHRACAPVYFEERHRPOCED 424  
Qy 451 TKPAFVADHAEVRFVFGAFLKGDIVFEGATEEBEKLRSRKMKYATFARTGNPND 510  
Db 425 -----BGATEEBEKLRSRKMKYATFARTGNPND 454  
Qy 511 DLSMPAVNLTEOYLQDLNMSLGQRLKEPRVDFTSTIPLIISASDMLHSPISLFTLS 570  
Db 455 DLSMPAVNLTEOYLQDLNMSLGQRLKEPRVDFTSTIPLIISASDMLHSPISLFTLS 514  
Qy 571 LLOPPFFCAP 581  
Db 515 LLOPPFFCAP 525

## RESULT 8

US-10-114-270-196

Sequence 196, Application US/10114270

Publication No. US2004003010A1

## GENERAL INFORMATION:

APPLICANT: Guo, Xiaojia  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Miller, Charles E.  
APPLICANT: Malyanekar, Uriel M.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Paturajan, Meera  
APPLICANT: Liu, Zhaohong  
APPLICANT: Gusev, Vladimir Y.  
APPLICANT: Li, Li  
APPLICANT: Vernet, Corine  
APPLICANT: Zernhusen, Bryan D.  
APPLICANT: Gorman, Linda  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Pena, Carol E.A.  
APPLICANT: Smithson, Glenda  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Shinkets, Richard A.  
APPLICANT: Gangoli, Bha A.  
APPLICANT: Taupier Jr., Raymond J.  
APPLICANT: Caeman, Stacie J.  
APPLICANT: Ji, Weizhen  
APPLICANT: Anderson, David W.  
APPLICANT: Liette, Mario W.  
APPLICANT: Raetelli, Luca  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Stone, David J.  
APPLICANT: Macdougall, John R.  
APPLICANT: Rothenberg, Mark E.  
TITLE OF INVENTION: NO. US20040030110A1 Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-322C  
CURRENT APPLICATION NUMBER: US/10/114,270  
CURRENT FILING DATE: 2002-11-27  
PRIOR APPLICATION NUMBER: 60/281,086  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/281,136  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/281,863  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/281,906

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; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SEQ ID NO 196
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-270-196

```

```

Query Match      84.4%; Score 2597.5; DB 15; Length 581;
Best Local Similarity 94.3%; Pred. No. 8.8e-233;
Matches 497; Conservative 4; Mismatches 17; Indels 9; Gaps 3;

```

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QY 31 GPSAEGPQRTNRLGWIQKQVTVLGSPPVNVFLGVPPAAPPGLSLRTTNPQASPMDNL 90
DB 27 GPSAEGPQRTNRLGWIQKQVTVLGSPPVNVFLGVPPAAPPGLSLRTTNPQASPMDNL 86
QY 91 REATSYPNCLQNSEWLLDDQMLKVHPKFGVSDCLYLNITYAPAHADTSGKLPVLMVF 150
DB 87 REATSYPNCLQNSEWLLDDQMLKVHPKFGVSDCLYLNITYAPAHADTSGKLPVLMVF 146
QY 151 PGGAFTGSGASIFDGSALAAVEDVLVVVOYRLGIFGFTTWDQHPGNAFQDQVAALS 210
DB 147 PGGAFTGSGASIFDGSALAAVEDVLVVVOYRLGIFGFTTWDQHPGNAFQDQVAALS 206
QY 211 WQKNIIEFGDPSSVTTFGESAGAIYSVSLILSPMAKGLFHKAIMSGVAIIPYLEAHD 270
DB 207 WQKNIIEFGDPSSVTTFGESAGAIYSVSLILSPMAKGLFHKAIMSGVAIIPYLEAHD 266
QY 271 YEKSEDLQVVAHFCGNNSDSEALLRCLRTPKSKELLTTSQKTSFTRVVDGAFPPNEPL 330
DB 267 YEKSEDLQVVAHFCGNNSDSEALLRCLRTPKSKELLTTSQKTSFTRVVDGAFPPNEPL 326
QY 331 DLSQKAFKAIPIIIGVNNHCGFLPMKE--APEILSGSNKSLAL-----HLIQIILHI 383
DB 327 DLSQKAFKAIPIIIGVNNHCGFLPMKE--APEILSGSNKSLAL-----HLIQIILHI 384
QY 384 PPOYLHIVANBYFPHDKSLTEIRDSLLDLGDFVFPVVPALITARYRDAGAPVYEFRRH 443
DB 385 PPOYLHIVANBYFPHDKSLTEIRDSLLDLGDFVFPVVPALITARYRDAGAPVYEFRRH 444
QY 444 PPOCFEDTKPAFYKAHDADEVRFVFGAFLKGDIVMFEAGATEEKLRSKMMKYATPAR 503
DB 445 PPOCFEDTKPAFYKAHDADEVRFVFGAFLKGDIVMFEAGATEEKLRSKMMKYATPAR 504
QY 504 TGNPNNDLSIMAYNLTLEYLQDLNMSLQORLKEPRVDFTSTIP 550
DB 505 TGNPNNDLSIMAYNLTLEYLQDLNMSLQORLKEPRVDFTSTIP 551

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RESULT 9
US-10-381-898-2
; Sequence 2, Application US/10381898
; Publication No. US2004008687A1
; GENERAL INFORMATION:
; APPLICANT: AZIMZAI, Yalda; BAUGHN, Mariah R.;
; APPLICANT: BOROMSKY, Mark L.; DING, Li;
; APPLICANT: DUGGAN, Brendan; ELIOTT, Vicki S.;
; APPLICANT: GANDHI, Ameena R.; GRIFFIN, Jennifer A.;
; APPLICANT: HAPALIA, April J.A.; ISON, Craig H.;
; APPLICANT: KHAN, Farrah A.; LAL, Preeti G.;

```

```

; APPLICANT: LEE, Ernestine A.; LU, Dying Alina M.;
; APPLICANT: ARVIZU, Chandra S.; POLICKY, Jennifer L.;
; APPLICANT: SANKUMAR, Jayalaxmi; RING, HuiJun Z.;
; APPLICANT: SAMJANWALA, Madhusudan M.;
; APPLICANT: TANG, Y. Tom; TRIBULEY, Catherine M.;
; APPLICANT: CHAMLA, Narinder K.; WALSH, Roderick T.;
; APPLICANT: WAREEN, Bridget; XU, Yuming;
; TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
; FILE REFERENCE: PI-0233 USN
; CURRENT APPLICATION NUMBER: US/10/381,898
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/US01/30662
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,947
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/238,864
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/242,323
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/247,581
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/249,519
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/252,834
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/250,567
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7473645CD1
US-10-381-898-2

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Query Match      84.1%; Score 2588.5; DB 15; Length 618;
Best Local Similarity 94.4%; Pred. No. 6.6e-232;
Matches 491; Conservative 1; Mismatches 5; Indels 23; Gaps 1;

```

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QY 31 GPSAEGPQRTNRLGWIQKQVTVLGSPPVNVFLGVPPAAPPGLSLRTTNPQASPMDNL 90
DB 92 GPSAEGPQRTNRLGWIQKQVTVLGSPPVNVFLGVPPAAPPGLSLRTTNPQASPMDNL 151
QY 91 REATSYPNCLQNSEWLLDDQMLKVHPKFGVSDCLYLNITYAPAHADTSGKLPVLMVF 150
DB 152 REATSYPNCLQNSEWLLDDQMLKVHPKFGVSDCLYLNITYAPAHADTSGKLPVLMVF 211
QY 151 PGGAFTGSGASIFDGSALAAVEDVLVVVOYRLGIFGFTTWDQHPGNAFQDQVAALS 210
DB 212 PGGAFTGSGASIFDGSALAAVEDVLVVVOYRLGIFGFTTWDQHPGNAFQDQVAALS 271
QY 211 WQKNIIEFGDPSSVTTFGESAGAIYSVSLILSPMAKGLFHKAIMSGVAIIPYLEAHD 270
DB 272 WQKNIIEFGDPSSVTTFGESAGAIYSVSLILSPMAKGLFHKAIMSGVAIIPYLEAHD 331
QY 271 YEKSEDLQVVAHFCGNNSDSEALLRCLRTPKSKELLTTSQKTSFTRVVDGAFPPNEPL 330
DB 332 YEKSEDLQVVAHFCGNNSDSEALLRCLRTPKSKELLTTSQKTSFTRVVDGAFPPNEPL 391
QY 331 DLSQKAFKAIPIIIGVNNHCGFLPM-----HIPOYLHL 428
DB 392 DLSQKAFKAIPIIIGVNNHCGFLPM-----HIPOYLHL 428
QY 391 VANEYFPHDKSLTEIRDSLLDLGDFVFPVVPALITARYRDAGAPVYEFRRPOCFED 450
DB 429 VANEYFPHDKSLTEIRDSLLDLGDFVFPVVPALITARYRDAGAPVYEFRRPOCFED 488
QY 451 TKPAFYKAHDADEVRFVFGAFLKGDIVMFEAGATEEKLRSKMMKYATPAR 510

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Db 469 TKPAAVKAADHAEVRFVFGAFLKGDIVMEGATEBEKLSRKMKYATPARTGNPNCN 548  
Qy 511 DLSLWPAVNLTEQYQLQDLNMSLGQRLKEPRVDFTWSTIP 550  
Db 549 DLSLWPAVNLTEQYQLQDLNMSLGQRLKEPRVDFTWSTIP 588

RESULT 10  
US-10-104-047-2219  
; Sequence 2219, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104, 047  
; PRIOR FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 2219  
; LENGTH: 469  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-047-2219

Query Match 79.7%; Score 2454; DB 15; Length 469;  
Best Local Similarity 99.6%; Pred. No. 15e-219;  
Matches 467; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 113 MLKVHYPKGVSEDCIYLNIVAPAHADTGSKLPVLVWPFPGAFTGSAIPDGSALAAVE 172  
Db 1 MLKVHYPKGVSEDCIYLNIVAPAHADTGSKLPVLVWPFPGAFTGSAIPDGSALAAVE 60  
Qy 173 DVLVVVVQYRLGIFGFTTWDQHPGNMAFKDQVAALSVQKNIIEFGGDPSSVTIIFGSS 232  
Db 61 DVLVVVVQYRLGIFGFTTWDQHPGNMAFKDQVAALSVQKNIIEFGGDPSSVTIIFGSS 120  
Qy 223 ACAISVSSILSPMAKGLFHAKIMESGVAIIPYLEADHDEKSEDIQVVAHFGGNASDSE 292  
Db 121 ACAISVSSILSPMAKGLFHAKIMESGVAIIPYLEADHDEKSEDIQVVAHFGGNASDSE 180  
Qy 293 ALLRCARTPKSEKELLTISOXTKSFTRVVDGAFFPNEPDLDSOKAFKAIPSIIGVNNHEC 352  
Db 181 ALLRCARTPKSEKELLTISOXTKSFTRVVDGAFFPNEPDLDSOKAFKAIPSIIGVNNHEC 240  
Qy 353 GFLLPKKEAPEILSGSNKSLALHLIQNLHIPPQYLAHVANEYFHDKSLTEIRDSLLDL 412  
Db 241 GFLLPKKEAPEILSGSNKSLALHLIQNLHIPPQYLAHVANEYFHDKSLTEIRDSLLDL 300  
Qy 413 LGDVFVVVVALTTAAYHRDAGAPVYFYEFRHRPQCEDEOTKPAFVADHAEVRFVFGAF 472  
Db 301 LGDVFVVVVALTTAAYHRDAGAPVYFYEFRHRPQCEDEOTKPAFVADHAEVRFVFGAF 360  
Qy 473 LKGDIVMEGATEBEKLSRKMKYATPARTGNPNCNLSLWPAVNLTEQYQLQDLNMS 532  
Db 361 LKGDIVMEGATEBEKLSRKMKYATPARTGNPNCNLSLWPAVNLTEQYQLQDLNMS 420  
Qy 533 LGQRLKEPRVDFTWSTIPIILSASDMLHSPSSLTFLSLQPFPPFCAP 581  
Db 421 LGQRLKEPRVDFTWSTIPIILSASDMLHSPSSLTFLSLQPFPPFCAP 469

RESULT 11  
US-10-233-933A-2  
; Sequence 2, Application US/10233933A  
; Publication No. US20040214171A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamashita, Tetsuro  
; APPLICANT: Miyazaki, Masao  
; TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER  
; FILE REFERENCE: SHIG FP02US006  
; ORGANISM: SHIG FP02US006

; CURRENT APPLICATION NUMBER: US/10/233, 933A  
; CURRENT FILING DATE: 2002-09-03  
; PRIOR APPLICATION NUMBER: JP2002-057908  
; PRIOR FILING DATE: 2002-04-03  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 542  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-10-233-933A-2

Query Match 64.5%; Score 1985; DB 16; Length 542;  
Best Local Similarity 71.7%; Pred. No. 1e-175;  
Matches 373; Conservative 60; Mismatches 85; Indels 2; Gaps 2;

Qy 31 GPSAAGPQNRIRIGIOGQVTVLGSPPVAVVFLGVPAAPIGLSRTNPSPASPMNDL 90  
Db 22 GPADAPVSTRIGLVNRKQTTVLGTVVNMFLGIPYAAPLGLRKRQKPKALPGNDF 81  
Qy 91 REATSYPNLCLQNSEMLLDQHMLKVHYPKGVSEDCIYLNIVAPAHADTGSKLPVLVWF 150  
Db 82 RNATSYPNLCLQNSEMLLVSYQHVLRKVPKLEASDCIYLNIVAPAHADNCSNLPVWVF 141  
Qy 151 PGGAFTGSAIPDGSALAAVEVDVLVVVVQYRLGIFGFTTWDQHPGNMAFKDQVAALS 210  
Db 142 PGGAFTGSAIPDGSALAAVEVDVLVVVVQYRLGIFGFTTWDQHPGNMAFKDQVAALS 201  
Qy 211 WVQKNIIEFGGDPSSVTIIFGSAAGISVSSILSPMAKGLFHAKIMESGVAIIPYL-BAH 269  
Db 202 WVQKNIIEFGGDPSSVTIIFGSAAGISVSSILSPMAKGLFHAKIMESGVAIIPYL-BAH 261  
Qy 270 DYKSESDQVVAHFGGNASDSEALLRCARTPKSEKELLTISOXTKSFTRVVDGAFFPNEP 329  
Db 262 GDERKQDQVLAIRICGCAASDASALLOCLRAKPSSELMIDISKULFSPVIDDFPPDBP 321  
Qy 330 LDLSOKAFKAIPSIIGVNNHECGFLPKKEAPEILSGSNKSLALHLIQNLHIPPQYLAH 389  
Db 322 VALLTQKAFNSVPSIIGVNNHECAFL-STEFSSEILSGSNKSLALYLVHTFANIPTQYLAH 380  
Qy 390 LVANEYFHDKSLTEIRDSLLDLGQDVFFVVPALTTAAYHRDAGAPVYFYEFRHRPQCE 449  
Db 381 LVADHYFYNKSPVSEIRDSFLDLGQDVFFVVPALTTAAYHRDAGAPVYFYEFRHRPQCE 440  
Qy 450 DTKPAFVADHAEVRFVFGAFLKGDIVMEGATEBEKLSRKMKYATPARTGNPNCN 509  
Db 441 DTKPAFVADHAEVRFVFGAFLKGDIVMEGATEBEKLSRKMKYATPARTGNPNCN 500  
Qy 510 NDLSPAVNLTEQYQLQDLNMSLGQRLKEPRVDFTWSTI 549  
Db 501 EGVLPMPAYTQSEQYQLKDLISVSVQKLEQVEEFMNTTI 540

RESULT 12  
US-10-233-933A-4  
; Sequence 4, Application US/10233933A  
; Publication No. US20040214171A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamashita, Tetsuro  
; APPLICANT: Miyazaki, Masao  
; TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER  
; FILE REFERENCE: SHIG FP02US006  
; CURRENT APPLICATION NUMBER: US/10/233, 933A  
; PRIOR FILING DATE: 2002-09-03  
; PRIOR APPLICATION NUMBER: JP2002-057908  
; PRIOR FILING DATE: 2002-04-03  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 542  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-10-233-933A-4

```

Query Match      64.5%; Score 1985; DB 16; Length 542;
Best Local Similarity 71.7%; Pred. No. 1e-175;
Matches 373; Conservative 60; Mismatches 85; Indels 2; Gaps 2;

QY 31 GPSAEGPQNTRLGWTGKQVTVLGSPPVNVFLGVFPAPPLGSLRFTNPQAPSPMDL 90
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 22 GFAADAPVATLGLWVRGKQTVLGSPPVNVFLGVFPAPPLGSLRFTNPQAPSPMDL 81
QY 91 REATSPNLCIQNSEMLLDQMLKVRYPKFGVSEDCVLYNAPAHADTSGKLPVLVWF 150
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 82 RNATSPYKLCFQDLEWLVSYQVHLKVRYPKLEASEDCVLYNAPAHADTSGKLPVLVWF 141
QY 151 PGGAFTGASAFIDSSALAAVEDVLYVNVQYRLGTFGFTTWDOHAPGNMAFKQVAAIS 210
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 142 PGGAFTGASAFIDSSALAAVEDVLYVNVQYRLGTFGFTTWDOHAPGNMAFKQVAAIS 201
QY 211 WVKNIIEFGGDPSSVTTFGESAGAISSVSLISPMAGLFPKKAIMEGVAIIYVL-EAH 269
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 202 WVRNDIEFGGDPSSVTTFGESAGAISSVSLISPMAGLFPKKAIMEGVAIIYVL-EAH 261
QY 270 DYKSEDDQVVAHFCCGNASDSEALLRCLRTKPSKELLTTSQTKSPFRVVDGAFPPNEP 329
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 262 GDERKCDQVLAIRICGCHASDSEALLRCLRTKPSKELLTTSQTKSPFRVVDGAFPPNEP 321
QY 330 LDLSQKAFKAIPTIIGVNHCEGFLPMKEAPETLSSGNSKSLAHLIQNLHITPQYLH 389
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 322 VALTQKAFNSVPSIIGVNHCEGFLPMKEAPETLSSGNSKSLAHLIQNLHITPQYLH 380
QY 390 LVANEYFHDKSLTEIRDSDLGLGVFVVPALITARYHDAGAPYFVEFRHRPQCFE 449
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 381 LVADHYFNKHSPEIRDSFLDLGDLVFPVGVVYARHDAQAPYFVEFRHRPQCFE 440
QY 450 DTKAFVYADADVRPFGAFPLKGDIVMEFGATEBEKLSRMMKYMTATPARTGPNNG 509
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 441 DTRPAFYVADSDIRFVFGAFPLKGDIVMEFGATEBEKLSRMMKYMTATPARTGPNNG 500
QY 510 NDLSMPAYNLTEQYLQDLNMSLGRLEKEPRVDFMTSTI 549
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 501 EGVPLMFAIYQSEYQLDLNMSLGRLEKEPRVDFMTSTI 540

RESULT 13
US-10-451-168-93
; Sequence 93, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50039
; CURRENT APPLICATION NUMBER: US/10/451,168
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/US01/49232
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,710
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/257,048
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/260,482
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/264,922
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/266,797
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/276,988
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/281,535
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/289,622
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 110

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-451-168-93

Query Match      57.8%; Score 1780; DB 15; Length 356;
Best Local Similarity 100.0%; Pred. No. 7.1e-157;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 IISPMAGLFPKKAIMEGVAIIIPYLEAHDKSEDDQVVAHFCCGNASDSEALLRCLRTK 301
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 17 IISPMAGLFPKKAIMEGVAIIIPYLEAHDKSEDDQVVAHFCCGNASDSEALLRCLRTK 76
QY 302 PSKEELLTTSQTKSPFRVVDGAFPPNEPDLISQKAFKAIPTIIGVNHCEGFLPMKEA 361
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 77 PSKEELLTTSQTKSPFRVVDGAFPPNEPDLISQKAFKAIPTIIGVNHCEGFLPMKEA 136
QY 362 PETLSSGNSKSLAHLIQNLHITPQYLH-VANEYFHDKSLTEIRDSDLGLGVFVVP 421
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 137 PETLSSGNSKSLAHLIQNLHITPQYLH-VANEYFHDKSLTEIRDSDLGLGVFVVP 196
QY 422 ALITARYHDAGAPYFVEFRHRPQCFEDTKPAFYKADHAEVRFVFGAFPLKGDIVME 481
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 197 ALITARYHDAGAPYFVEFRHRPQCFEDTKPAFYKADHAEVRFVFGAFPLKGDIVME 256
QY 482 GATBEKLSRMMKYMTATPARTGPNNGNDLSMPAYNLTEQYLQDLNMSLGRLEKEPR 541
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 257 GATBEKLSRMMKYMTATPARTGPNNGNDLSMPAYNLTEQYLQDLNMSLGRLEKEPR 541
QY 542 VDFMTSTIPLISASDMLHSPSLTFLSLQPFEEFCAP 581
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 317 VDFMTSTIPLISASDMLHSPSLTFLSLQPFEEFCAP 356

RESULT 14
US-09-925-298-689
; Sequence 689, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PAL03
; CURRENT APPLICATION NUMBER: US/09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 689
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-298-689

Query Match      39.9%; Score 1230; DB 9; Length 549;
Best Local Similarity 46.7%; Pred. No. 2.6e-105;
Matches 248; Conservative 91; Mismatches 168; Indels 24; Gaps 8;

QY 31 GPSAEGPQNTRLGWTGKQVTVLGSPPVNVFLGVFPAPPLGSLRFTNPQAPSPMDL 90
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 16 GQDSASPIRTHTGTVLGSVHVKGANAGVQTFLLGIPAKPLGLRFPAPPPSSWSGV 75

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QY 91 REATSYNCLON-----SEWLLDQHLKHYPKFVSEDCLYNTYAPAHADTGSKL 145
DB 76 RDGTHPAMCLODITAVESEFL-----SOFNMTFSPDSMSEDCLYSTYTPAHSHSGSNLP 131
QY 146 VLWVFGGAFKTSASIFPGSALAAVEDLVVVVYRIGIFGFPTWDOHAPGNWAFDX 205
DB 132 VVVVHGGALVFGMASLVDGSMALABENVVVIIQYRGLVGFSTGDHATGNMGYLDQ 191
QY 206 VAALSWQKNIIEFGGDPSSVTITFESAGALSVSSLLISPMAGLFFHKAIMESGVAIIPY 265
DB 192 VAALRWQONIAHFGGNPDRTYITFESAGTSVSVSLVSPISQGLFHGAIMESGVALLPG 251
QY 266 LEADHYKSEDL--QVVAHFGGNASDSEALIRCLRTPKSKELLTSGKTSFTYVNDGA 323
DB 252 LIA-----SSADVISTVVAHLSACDQVDSSEALVGLRGKSKEILAINKPFKMI PGVVDGV 307
QY 324 FFPNEPDLISOKAFKAIPTIIGVNNHCEGFLP-----MKEAPETLSGNSKSLALHLION 379
DB 308 FLPRHPQELIASADQOPVPSIVGVNNNEFGWLI PKVMRIYDTQKEMDEASQALQKMLT 367
QY 360 ILHIPOYLHLVANEYFHDKHSLTEIRDSLDDLGDVFFVVPALITARYHRDAGAPVYFY 439
DB 368 LLMLEPTFGDLREBYIGDNGDPQTLQAQOFEMMADSMFVIPALQVAHF--QCSRAPVYFY 426
QY 440 EFRHRPOCFEDTKPAFVYKADHAEVRFYFGAFLKGDIVMEGATEEEXLSRKMKTWA 499
DB 427 EFOHQPMSWKNIIRPHMKADHGDDEL.PFVF-RSFGGNVYIKF--TEEBEQLSRKMKTWA 482
QY 500 TPARTGNNGNDLSMPAYNLTEOYLQDLNMSLQORLKEPRVDFTWSTIP 550
DB 483 NFARNGNPGEGLPHMPL.FDOEBOYLQNLQPAVGRALKAHRLQFWKCALP 533

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## RESULT 15

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US-10-102-806-689
; Sequence 689, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 689
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-689

```

```

Query Match 39.9%; Score 1230; DB 14; Length 549;
Best Local Similarity 46.7%; Pred. No. 2,6e-105;
Matches 248; Conservative 91; Mismatches 168; Indels 24; Gaps 8;

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```

QY 31 GPSABGQNTLGLWQGVYVSGPVVNVN/FLGVFAAPLGLSFTNPPQASPMNDL 90
DB 16 GODSASPIRTHTTGOVLGSLVHKGANAGVQTLGIPFAKPPGLRFAPEEPESWGSV 75
QY 91 REATSYNCLON-----SEWLLDQHLKHYPKFVSEDCLYNTYAPAHADTGSKL 145

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DB 76 RDGTHPAMCLODITAVESEFL-----SOFNMTFSPDSMSEDCLYSTYTPAHSHSGSNLP 131
QY 146 VLWVFGGAFKTSASIFPGSALAAVEDLVVVVYRIGIFGFPTWDOHAPGNWAFDX 205
DB 132 VVVVHGGALVFGMASLVDGSMALABENVVVIIQYRGLVGFSTGDHATGNMGYLDQ 191
QY 206 VAALSWQKNIIEFGGDPSSVTITFESAGALSVSSLLISPMAGLFFHKAIMESGVAIIPY 265
DB 192 VAALRWQONIAHFGGNPDRTYITFESAGTSVSVSLVSPISQGLFHGAIMESGVALLPG 251
QY 266 LEADHYKSEDL--QVVAHFGGNASDSEALIRCLRTPKSKELLTSGKTSFTYVNDGA 323
DB 252 LIA-----SSADVISTVVAHLSACDQVDSSEALVGLRGKSKEILAINKPFKMI PGVVDGV 307
QY 324 FFPNEPDLISOKAFKAIPTIIGVNNHCEGFLP-----MKEAPETLSGNSKSLALHLION 379
DB 308 FLPRHPQELIASADQOPVPSIVGVNNNEFGWLI PKVMRIYDTQKEMDEASQALQKMLT 367
QY 360 ILHIPOYLHLVANEYFHDKHSLTEIRDSLDDLGDVFFVVPALITARYHRDAGAPVYFY 439
DB 368 LLMLEPTFGDLREBYIGDNGDPQTLQAQOFEMMADSMFVIPALQVAHF--QCSRAPVYFY 426
QY 440 EFRHRPOCFEDTKPAFVYKADHAEVRFYFGAFLKGDIVMEGATEEEXLSRKMKTWA 499
DB 427 EFOHQPMSWKNIIRPHMKADHGDDEL.PFVF-RSFGGNVYIKF--TEEBEQLSRKMKTWA 482
QY 500 TPARTGNNGNDLSMPAYNLTEOYLQDLNMSLQORLKEPRVDFTWSTIP 550
DB 483 NFARNGNPGEGLPHMPL.FDOEBOYLQNLQPAVGRALKAHRLQFWKCALP 533

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Search completed: June 16, 2005, 20:58:35
Job time : 163 secs

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CC related disorders. A claimed method of treating or preventing a disorder  
 CC (especially a pain-related disorder) characterised by aberrant activity  
 CC of a 53010-expressing cell involves administering a compound that  
 CC modulates 53010 activity or expression  
 XX

Sequence 581 AA;

Query Match 100.0%; Score 581; DB 5; Length 581;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MPOGLTSSASQWCFLLIQPLIGHROMKGTGPSAGPQNTLGMIOGKQVTVLGSPPV 60
DB 1 MPOGLTSSASQWCFLLIQPLIGHROMKGTGPSAGPQNTLGMIOGKQVTVLGSPPV 60
QY 61 NVFLGVFAAPPLGSLRFTNPQASPMWDLREATSYPNLCLQNSWLLLDQHLKVHYPK 120
DB 61 NVFLGVFAAPPLGSLRFTNPQASPMWDLREATSYPNLCLQNSWLLLDQHLKVHYPK 120
QY 121 FGVSEDCLYNIIYAPAHADTGSKLPLYVWFPFGAFKTSASIFDGSALAAYEDVLVVVQ 180
DB 121 FGVSEDCLYNIIYAPAHADTGSKLPLYVWFPFGAFKTSASIFDGSALAAYEDVLVVVQ 180
QY 181 YRLGIFGEFTTMDQHPGNMAFKDOVAALSWQKIEFFGDPSSVTTFGSAGAISSVS 240
DB 181 YRLGIFGEFTTMDQHPGNMAFKDOVAALSWQKIEFFGDPSSVTTFGSAGAISSVS 240
QY 241 LILSPMAKGLFHKAIMESGVAIIPYLEADHYEKSEDLQVVAFCGNNAOSEALLRCLRT 300
DB 241 LILSPMAKGLFHKAIMESGVAIIPYLEADHYEKSEDLQVVAFCGNNAOSEALLRCLRT 300
QY 301 KPSKELLTSSQKTSFTRVVDGAFPPNEPLDLSQKAFKAIPSIIGVNNHECGFLPMKE 360
DB 301 KPSKELLTSSQKTSFTRVVDGAFPPNEPLDLSQKAFKAIPSIIGVNNHECGFLPMKE 360
QY 361 APEILSGNKSALHLIQLNIHIPPQYHLVANEYFHDKSLTIRPSLDLGDVFFV 420
DB 361 APEILSGNKSALHLIQLNIHIPPQYHLVANEYFHDKSLTIRPSLDLGDVFFV 420
QY 421 PALITARYHRDAGAPVYFYEFRHRPOCFEDTKPAFVADNADEVRFVFGAFLKGDIVMF 480
DB 421 PALITARYHRDAGAPVYFYEFRHRPOCFEDTKPAFVADNADEVRFVFGAFLKGDIVMF 480
QY 481 EGATEEBEKLTSRKMMKWTATFARTGNPNDLSMPAYNLTEOYLQDLIMSLGOLKEP 540
DB 481 EGATEEBEKLTSRKMMKWTATFARTGNPNDLSMPAYNLTEOYLQDLIMSLGOLKEP 540
QY 541 RVDFWISTITPILISASDMLHSPSLTFTSLQPFPPFCAP 581
DB 541 RVDFWISTITPILISASDMLHSPSLTFTSLQPFPPFCAP 581

```

RESULT 2

ADQ89094  
 ADQ89094 standard; protein; 581 AA.

AC ADQ89094;

DT 21-OCT-2004 (first entry)

DE Human urological disorder related protein 53010 SEQ:46.

KW urological disorder; uropathic; cytostatic; urinary incontinence;

OS Homo sapiens.

PN MO2004065576-A2.

PD 05-AUG-2004.

PF 14-JAN-2004; 2004MO-US000750.

XX

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PR 15-JAN-2003; 2003US-0440318P.
PR 04-FEB-2003; 2003US-0444783P.
PR 27-MAR-2003; 2003US-0457901P.
PR 08-MAY-2003; 2003US-0468775P.
PR 19-MAY-2003; 2003US-0471614P.
PR 16-JUN-2003; 2003US-0478742P.
PR 18-JUL-2003; 2003US-0488529P.
PR 30-JUL-2003; 2003US-0491156P.
PR 02-SEP-2003; 2003US-0495954P.
PR 26-SEP-2003; 2003US-0506332P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Karicheti V, Silos-Santiago I, Eliasef SD;
PI WPI, 2004-562167/54.
XX N-PSDB; ADQ89093.
XX
XX Use of polypeptides related to urological disorders, e.g. 44390, 54181,
PT 211 or for identifying a compound capable of treating a urological
PT disorder or identifying and treating a subject having a urological
XX disorder.
XX
XX claim 1; SEQ ID NO 46; 542pp; English.
XX
XX The present invention describes the use of polypeptides related to
CC urological disorders for identifying a compound capable of treating a
CC urological disorder, identifying a subject having a urological disorder,
CC or treating a subject having a urological disorder. Also described: (1) a
CC method for identifying a compound capable of treating a urological
CC disorder; (2) a method for identifying a subject having a urological
CC disorder; and (3) a method for treating a subject having a urological
CC disorder. The compound has uropathic and cytostatic activities. The
CC compound is related to urological disorders are useful for identifying a
CC compound capable of treating a urological disorder, identifying a subject
CC having a urological disorder, or treating a subject having a urological
CC disorder. Disorders include urinary incontinence and benign prostatic
CC hyperplasia. The present sequence represents a human urological disorder
CC related protein, which is used in the exemplification of the present
XX invention.
XX
XX Sequence 581 AA;

```

Query Match 100.0%; Score 581; DB 8; Length 581;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MPOGLTSSASQWCFLLIQPLIGHROMKGTGPSAGPQNTLGMIOGKQVTVLGSPPV 60
DB 1 MPOGLTSSASQWCFLLIQPLIGHROMKGTGPSAGPQNTLGMIOGKQVTVLGSPPV 60
QY 61 NVFLGVFAAPPLGSLRFTNPQASPMWDLREATSYPNLCLQNSWLLLDQHLKVHYPK 120
DB 61 NVFLGVFAAPPLGSLRFTNPQASPMWDLREATSYPNLCLQNSWLLLDQHLKVHYPK 120
QY 121 FGVSEDCLYNIIYAPAHADTGSKLPLYVWFPFGAFKTSASIFDGSALAAYEDVLVVVQ 180
DB 121 FGVSEDCLYNIIYAPAHADTGSKLPLYVWFPFGAFKTSASIFDGSALAAYEDVLVVVQ 180
QY 181 YRLGIFGEFTTMDQHPGNMAFKDOVAALSWQKIEFFGDPSSVTTFGSAGAISSVS 240
DB 181 YRLGIFGEFTTMDQHPGNMAFKDOVAALSWQKIEFFGDPSSVTTFGSAGAISSVS 240
QY 241 LILSPMAKGLFHKAIMESGVAIIPYLEADHYEKSEDLQVVAFCGNNAOSEALLRCLRT 300
DB 241 LILSPMAKGLFHKAIMESGVAIIPYLEADHYEKSEDLQVVAFCGNNAOSEALLRCLRT 300
QY 301 KPSKELLTSSQKTSFTRVVDGAFPPNEPLDLSQKAFKAIPSIIGVNNHECGFLPMKE 360
DB 301 KPSKELLTSSQKTSFTRVVDGAFPPNEPLDLSQKAFKAIPSIIGVNNHECGFLPMKE 360
QY 361 APEILSGNKSALHLIQLNIHIPPQYHLVANEYFHDKSLTIRPSLDLGDVFFV 420
DB 361 APEILSGNKSALHLIQLNIHIPPQYHLVANEYFHDKSLTIRPSLDLGDVFFV 420

```

Db 361 APELSSGSKSLAHLNIIHIPQYHLVANEYFHDKSLTERDSDLGDFVTV 420  
Qy 421 PALITARYHRDAGAVVYEFERHPOCEDTKPAFVKADHDEVFVFGAFLKGDIMWF 480  
Db 421 PALITARYHRDAGAVVYEFERHPOCEDTKPAFVKADHDEVFVFGAFLKGDIMWF 480  
Qy 481 EGATEEERKLSRKMMKYATPARGTNGNDLSLWPAYNLTEQYQLDLNLSLGRLEP 540  
Db 481 EGATEEERKLSRKMMKYATPARGTNGNDLSLWPAYNLTEQYQLDLNLSLGRLEP 540  
Qy 541 RVDFWTSTPILSLASDMLHSPSLSTPLSLQPFPCAP 581  
Db 541 RVDFWTSTPILSLASDMLHSPSLSTPLSLQPFPCAP 581  
RESULT 3  
ABP61004  
ID ABP61004 standard; protein; 575 AA.  
AC ABP61004;  
XX  
XX 10-SEP-2002 (first entry)  
XX  
XX Novel human protein. SEQ ID 91.  
XX  
XX Human; cytosolic; vulnery; antiarteriosclerotic; antiparkinsonian;  
XX nootropic; neuroprotective; immunosuppressive; haemostatic;  
XX antiinflammatory; cardiant; antilicer; virucide; antithyroid;  
XX cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;  
XX wound healing disorders; atherosclerosis; Parkinson's disease;  
XX Alzheimer's disease; autoimmune disorder; haematopoietic disorder;  
XX inflammation; neoplastic disease; nervous system disorder;  
XX cardiovascular disorders; pancreatitis; respiratory disorder;  
XX hyperproliferation; systemic autoimmune disease; hyper-immunity;  
XX developmental abnormality; gastrointestinal ulceration; neuropathy;  
XX haematological disease; metabolic disease; sperm dysfunction;  
XX thyroid disorder; hypothyroidism; brain damage; colitis;  
XX cone photo-transduction deficiency; neurological disease; stroke;  
XX angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;  
XX trachea; thymus; lymph node; muscular system; obesity; anorexia;  
XX growth abnormality; precocious puberty.  
XX  
XX Homo sapiens.  
XX OS  
XX WO200250105-A1.  
XX  
XX 27-JUN-2002.  
XX  
XX 17-DEC-2001; 2001WO-US049232.  
XX  
XX 19-DEC-2000; 2000US-0256710P.  
XX 20-DEC-2000; 2000US-0257048P.  
XX 09-JAN-2001; 2001US-0260482P.  
XX 30-JAN-2001; 2001US-0264922P.  
XX 06-FEB-2001; 2001US-0266797P.  
XX 19-MAR-2001; 2001US-0276988P.  
XX 04-APR-2001; 2001US-0281535P.  
XX 08-MAY-2001; 2001US-0289622P.  
XX  
XX (SMK) SMITHKLINE BEECHAM CORP.  
XX PA (SMK) SMITHKLINE BEECHAM PLC.  
XX PA (GLAX) GLAXO GROUP LTD.  
XX  
XX Agarwal P, Birkeland M, Cogswell JP, Kahnack KP, Lai Y;  
XX Martensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q;  
XX WPI; 2002-508784/54.  
XX DR N-PSDB; ABQ86169.  
XX  
XX Secreted proteins and polynucleotides useful as vaccines for preventing  
XX or treating various diseases e.g. cancer, wounds, atherosclerosis,  
XX Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.  
XX

PS Claim 1(a): Page 312-313; 335pp; English.  
XX  
XX The invention relates to an isolated polypeptide with signal sequences  
XX which allow it to be secreted extracellularly or membrane associated. The  
XX activity of polypeptides of the invention may be described as,  
XX cytosolic, vulnery, antiarteriosclerotic, antiparkinsonian, nootropic,  
XX neuroprotective, immunosuppressive, haemostatic, antiinflammatory,  
XX cardiant, antilicer, virucide, antithyroid, cerebroprotective, anorectic,  
XX and metabolic. Polypeptides and polynucleotides of the invention are  
XX useful in the treatment, or as a vaccine in the prevention of, cancer,  
XX wound healing disorders, infection, atherosclerosis, Parkinson's disease  
XX and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,  
XX inflammation, neoplastic diseases, nervous system related disorders and  
XX cardiovascular disorders, pancreatitis, respiratory disorder,  
XX hyperproliferation, systemic autoimmune disease, hyper-immunity,  
XX developmental abnormality, gastrointestinal ulceration, neuropathy,  
XX haematological diseases, metabolic diseases, sperm dysfunction, thyroid  
XX disorders e.g. hypothyroidism, brain damage, colitis, cone photo-  
XX transduction deficiency, neurological diseases, stroke, angiogenesis,  
XX ovulation disorders, diseases in the spinal cord, thyroid gland, heart,  
XX trachea, thymus, lymph node and muscular system, obesity, anorexia,  
XX growth abnormalities, and alleviation of precocious puberty. The  
XX sequences given in records ABP60965-ABP61019 represent novel human  
XX proteins of the invention  
XX  
XX Sequence 575 AA:  
XX  
XX Query Match 94.8%; Score 551; DB 5; Length 575;  
XX Best Local Similarity 100.0%; Pred. No. 0;  
XX Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 31 GPSAEGPQNRTRLMIGQKQYTVLGSPPVNVFLGVPAPPLGSLRFTNPQASPMWNL 90  
Db 25 GPSAEGPQNRTRLMIGQKQYTVLGSPPVNVFLGVPAPPLGSLRFTNPQASPMWNL 84  
Qy 91 REATSYPLCLQNSBWLDDHMKKHYPKRGVSEDCYINITYAPAHDTSSKLPVLMWF 150  
Db 85 REATSYPLCLQNSBWLDDHMKKHYPKRGVSEDCYINITYAPAHDTSSKLPVLMWF 144  
Qy 151 PGAFKTSASIFPGSALAAVEDYLVVVOYRLGIFGFTTMDQHPANMAFKQVALS 210  
Db 145 PGAFKTSASIFPGSALAAVEDYLVVVOYRLGIFGFTTMDQHPANMAFKQVALS 204  
Qy 211 WVKNIIEFFGDPSSVITFGESAGASVSSILSPMAKGLPHKAIMESGVAIIPYLEAND 270  
Db 205 WVKNIIEFFGDPSSVITFGESAGASVSSILSPMAKGLPHKAIMESGVAIIPYLEAND 264  
Qy 271 YEKSEDLQVNAHFCGNNADESEALLRCIRTPSKBLTLLSQITTSFTTVVVGAFPPNEPL 330  
Db 265 YEKSEDLQVNAHFCGNNADESEALLRCIRTPSKBLTLLSQITTSFTTVVVGAFPPNEPL 324  
Qy 331 DLSOKAFKAIPIIIVNNHSCGFLPMKEAPETLSSGSKSLAHLNIIHIPQYHL 390  
Db 325 DLSOKAFKAIPIIIVNNHSCGFLPMKEAPETLSSGSKSLAHLNIIHIPQYHL 384  
Qy 391 VANEYFHDKSLTEIRDSLDLGDVFEVVPALITARYHRDAGAVVYEFERHPOCED 450  
Db 385 VANEYFHDKSLTEIRDSLDLGDVFEVVPALITARYHRDAGAVVYEFERHPOCED 444  
Qy 451 TKPAFVKADHDEVFVFGAFLKGDIMWFEGATEEERKLSRKMMKYATPARGTNGN 510  
Db 445 TKPAFVKADHDEVFVFGAFLKGDIMWFEGATEEERKLSRKMMKYATPARGTNGN 504  
Qy 511 DLSLMPAYNLTEQYQLDLNLSLGRLEPVDWTSTPILSLASDMLHSPSLSTPLS 570  
Db 505 DLSLMPAYNLTEQYQLDLNLSLGRLEPVDWTSTPILSLASDMLHSPSLSTPLS 564  
Qy 571 LLQPFPCAP 581  
Db 565 LLQPFPCAP 575  
RESULT 4

AD54807  
ID AD54807 standard; protein; 525 AA.  
AC AD54807;  
XX  
XX  
XX 20-NOV-2003 (first entry)  
DT  
XX  
XX Human protein, SEQ ID 2375.  
DE  
XX  
XX Cytostatic; Anti-inflammatory; Osteoprotective; Neuroprotective; Nootropic;  
XX Gene Therapy; human; secretory protein; membrane proteins; cancer;  
XX inflammatory disease; osteoporosis; neurological disease.  
OS  
XX Homo sapiens.  
PN  
XX EP1293569-A2.  
XX  
XX 19-MAR-2003.  
PD  
XX  
XX 21-MAR-2002; 2002EP-00006586.  
PF  
XX  
XX 14-SEP-2001; 2001JP-00328381.  
PR 24-JAN-2002; 2002US-0350435P.  
XX  
XX (HELI-) HELIX RES INST.  
XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX  
XX  
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,  
PI Seki N, Toshihawa T, Otsuka M, Nagahari K, Maunho Y;  
XX WPI; 2003-395539/38.  
XX N-PSDB; AD53168.  
XX  
XX  
XX New polynucleotides encoding full-length polypeptides, e.g. secretory  
PT and/or membrane proteins, useful for developing medicines for diseases in  
PT which the gene is involved, or as target molecules for gene therapy.  
XX  
XX Claim 14; SEQ ID NO 2375; 205pp; English.  
XX  
XX The present invention relates to novel human secretory or membrane  
CC proteins (AD54072-AD55710) and their coding sequences (AD542433-  
CC AD544071). The coding sequences are useful in the gene therapy of  
CC diseases caused by abnormalities of the proteins, e.g. cancer,  
CC inflammatory diseases, osteoporosis or neurological disease.  
XX  
XX Sequence 525 AA;  
SQ  
Query Match 68.8%; Score 400; DB 6; Length 525;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 31 GPSAEGFORNTRLGWLQKQVTVLGSFVNVFLGVPPAPPLGSRFTNPPASPMWNL 90  
DB 25 GPSAEGFORNTRLGWLQKQVTVLGSFVNVFLGVPPAPPLGSRFTNPPASPMWNL 84  
QY 91 REATSVNCLQKQVTVLGSFVNVFLGVPPAPPLGSRFTNPPASPMWNL 150  
DB 85 REATSVNCLQKQVTVLGSFVNVFLGVPPAPPLGSRFTNPPASPMWNL 144  
QY 151 PGCAFRTGSAISIFDGSALAAEYDVLVVVQYRLGIFGFTTWDQAHAPGNMAFKQVVALS 210  
DB 145 PGCAFRTGSAISIFDGSALAAEYDVLVVVQYRLGIFGFTTWDQAHAPGNMAFKQVVALS 204  
QY 211 WVOXNIEFGGDPSSVTITGESAGAISSVLLISPMAGLFFKAIMESGVAILPYLEAHD 270  
DB 205 WVOXNIEFGGDPSSVTITGESAGAISSVLLISPMAGLFFKAIMESGVAILPYLEAHD 264  
QY 271 YKESBDLQVVAHFCCGNASDSEALRCURTSPKSLTLTSLQKTSFTRVVDGAFPEEPL 330  
DB 265 YKESBDLQVVAHFCCGNASDSEALRCURTSPKSLTLTSLQKTSFTRVVDGAFPEEPL 324  
QY 331 DLSQKAFKALPISITIGVNNHECGFLLPMKEAPEILSGSNKSLALHLQNLILHPQYLHL 390

DB 325 DLSQKAFKALPISITIGVNNHECGFLLPMKEAPEILSGSNKSLALHLQNLILHPQYLHL 384  
QY 391 VANEYFHDKSLTEIRDSLLDLGDFVFPVVPALITARYR 430  
DB 385 VANEYFHDKSLTEIRDSLLDLGDFVFPVVPALITARYR 424  
RESULT 5  
ID ABM84114 standard; protein; 642 AA.  
XX  
XX ABM84114;  
AC  
XX  
XX 18-NOV-2004 (first entry)  
DT  
XX  
XX Human diagnostic and therapeutic pprotein SEQ ID NO:4363.  
DE  
XX  
XX gene therapy; human diagnostic and therapeutic polynucleotide; dthp.  
KM  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004023973-A2.  
XX  
XX 25-MAR-2004.  
XX  
XX 12-SEP-2003; 2003WO-US028227.  
XX  
XX 12-SEP-2002; 2002US-0410259P.  
XX 12-SEP-2002; 2002US-0410260P.  
XX  
XX (INCY-) INCYTE CORP.  
XX  
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic NM, Shen F,  
PI Harnishorne TR, Suchorolski MT, Altus CM, Pitts SJ, Elder LV,  
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;  
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve DL;  
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitec UA, Kirtton ES;  
PI Xu Y, Kwong M, Policy JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,  
PI Patry S, Shi X, Suarez CJ;  
XX  
XX WPI; 2004-329368/30.  
XX N-PSDB; ACN42766.  
XX  
XX  
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.  
XX  
XX Claim 27; Page; 190pp; English.  
XX  
XX The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorders, developmental disorders,  
CC disorders, neurological disorders, gastrointestinal disorder, endocrine  
CC infections caused by virus, bacteria, fungi or parasite. The dthp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dthp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
XX  
XX Sequence 642 AA;  
SQ  
Query Match 67.3%; Score 391; DB 8; Length 642;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 TMDQAPGNMAFKQVAAALSWQKNIFFGGDPSSVTIFGSSAGAI SVSSLLSPMAGL 250

DB 252 TMDQAPGNMAFKQVAAALSWQKNIFFGGDPSSVTIFGSSAGAI SVSSLLSPMAGL 311

QY 251 FHKAIMESGVAIIPYLEAHDEKSEDLQVVAHFCGNNA SDSEALIRCLRTKPSKELLTLS 310

DB 312 FHKAIMESGVAIIPYLEAHDEKSEDLQVVAHFCGNNA SDSEALIRCLRTKPSKELLTLS 371

QY 311 OKTSSFTVVDGAFPPNEPLDLSOKAFRAI PSII GVNNHGCGFLPKKEAPEILSSGSK 370

DB 372 OKTSSFTVVDGAFPPNEPLDLSOKAFRAI PSII GVNNHGCGFLPKKEAPEILSSGSK 431

QY 371 SLALHILNIILHIPPQYHLVANEYFHDKHSLTEIRSDLLDGDVFPVPAALITARYHR 430

DB 432 SLALHILNIILHIPPQYHLVANEYFHDKHSLTEIRSDLLDGDVFPVPAALITARYHR 491

QY 431 DAGAFVYFEPHRRPQCEFDTPKPAFVKADHAEVRFVFGAFLKGDIVMEGATEEEKL 490

DB 492 DAGAFVYFEPHRRPQCEFDTPKPAFVKADHAEVRFVFGAFLKGDIVMEGATEEEKL 551

QY 491 SRKMKYATPARTNPNGNDLSLMPAYNLTPQYIQLDLNLSGRLKEPRDFTSTIP 550

DB 552 SRKMKYATPARTNPNGNDLSLMPAYNLTPQYIQLDLNLSGRLKEPRDFTSTIP 611

QY 551 LILSADMLHSPSLSTLTPSLLOPPFPFCAP 581

DB 612 LILSADMLHSPSLSTLTPSLLOPPFPFCAP 642

RESULT 6  
AAE25025  
ID AAE25025 standard; protein; 642 AA.

XX AAE25025;

DT 30-OCT-2002 (first entry)

XX Human drug metabolizing enzyme (DME-10).

XX Human; drug metabolizing enzyme; autoimmune; inflammatory disorder;  
XX acquired immunodeficiency syndrome; AIDS; atherosclerosis; psoriasis;  
XX proliferative disorder; arteriosclerosis; cirrhosis; hepatitis; cancer;  
XX asthma; neurological disorder; Alzheimer's disease; Huntington's disease;  
XX dementia; Parkinson's disease; developmental disorder; anaemia; adenoma;  
XX drug screening; endocrine disorder; conjunctivitis; glaucoma; cataract;  
XX renal tubular acidosis; eye disorder; epilepsy; thrombosis; peptic ulcer;  
XX anorexia; metabolic disorder; cystic fibrosis; diabetes; liver disorder;  
XX gastritis; gastrointestinal disorder; gene therapy; virulence; anticoagulant;  
XX anticonvulsant; nootropic; enzyme; DME-10.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..50

FT Domain /label= Signal\_peptide 32..56

FT Protein /note= "Transmembrane domain" 51..642

FT Domain /note= "Mature human DME-10" 113..135

FT Domain /note= "Transmembrane domain" 204..220

FT Domain /note= "Transmembrane domain" 234..250

FT Domain /note= "Transmembrane domain" 287..314

FT Domain /note= "Transmembrane domain" 463..491

XX /note= "Transmembrane domain"

WO200246426-A2.

XX 13-JUN-2002.

XX 04-DEC-2001; 2001WO-US047429.

XX 08-DEC-2000; 2000US-0254308P.

XX 15-DEC-2000; 2000US-0256189P.

XX 21-DEC-2000; 2000US-0257713P.

XX 19-JAN-2001; 2001US-0262706P.

XX 02-FEB-2001; 2001US-0266020P.

XX (INCY-) INCYTE GENOMICS INC.

XX Sanjanwala MM, Yao WG, Au-Young J, Baughn MR, Arvizu C, Ring HZ,  
XX Lee EA, Ding L, Hafalia AJA, Tang YT, Yue H, Tribouley CM, Lu DM,  
XX Lal PG, Warren BA, Yang J, Walla NK, Nguyen DB, Gandhi AR, Lu Y,  
XX Ison CH;  
XX WPI: 2002-519668/55.  
XX N-PSDB; AAD40574.

DR Novel human drug metabolizing polypeptide, useful in diagnosis,  
DR prevention or treatment of autoimmune/inflammatory, cell proliferative,  
PT neurological, developmental, endocrine, metabolic and gastrointestinal  
PT disorders.

PS Claim 65; Page 155-156; 169pp; English.

XX The invention relates to an isolated human drug metabolizing enzyme (DME)  
XX and its nucleotide. DME is useful for diagnosing, treating or preventing  
XX disorders associated with aberrant expression of DME, where the disorders  
XX are selected from autoimmune/inflammatory disorder such as acquired  
XX immunodeficiency syndrome (AIDS), asthma, atherosclerosis, psoriasis,  
XX uveitis; a cell proliferative disorder such as arteriosclerosis,  
XX cirrhosis, hepatitis, and cancer; a neurological disorder such as  
XX Alzheimer's disease, Huntington's disease, dementia, Parkinson's disease;  
XX a developmental disorder such as renal tubular acidosis, epilepsy,  
XX anaemia; an endocrine disorder such as adenoma, thrombosis and infections  
XX; an eye disorder such as conjunctivitis, glaucoma, cataract; metabolic  
XX disorder such as cystic fibrosis, diabetes and goitre; a gastrointestinal  
XX disorder such as anorexia, peptic ulcer; and liver disorders. DME is  
XX useful in a number of drug screening techniques and to analyse the  
XX proteome of a tissue or cell type. The invention is useful for creating  
XX knock-in humanised animals or transgenic animals to model human diseases,  
XX in somatic or germ-line gene therapy, to generate a transcript image of a  
XX tissue or cell type, for detecting differences in the chromosomal  
XX location due to translocation, inversion, etc. among normal, carrier or  
XX affected individuals, and as hybridisation probes for mapping naturally  
XX occurring genomic sequences. The present sequence is human DME-10

SO Sequence 642 AA;

Query Match 65.6%; Score 381; DB 5; Length 642;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 31 GPSAEGPORNRLGWIQGYVTVGSPVYVNVFLGVPAPPLGSLRTNPOPASPMNL 90

DB 92 GPSAEGPORNRLGWIQGYVTVGSPVYVNVFLGVPAPPLGSLRTNPOPASPMNL 151

QY 91 REATSYPTLCIONSEMLLDQMLKVHPKFGVSEDCILYNIYAPAHADTGSKLPLVWF 150

DB 152 REATSYPTLCIONSEMLLDQMLKVHPKFGVSEDCILYNIYAPAHADTGSKLPLVWF 211

QY 151 PGAFKTSASIPDGSALAAVEDVLYVVVQYRLGIFGFTTWDQAPGNMAFKQVAAALS 210

DB 212 PGAFKTSASIPDGSALAAVEDVLYVVVQYRLGIFGFTTWDQAPGNMAFKQVAAALS 271

QY 211 WQKNIFFGGDPSSVTIFGSSAGAI SVSSLLSPMAGL FHKAIMESGVAIIPYLEAHD 270

DB 272 WQKNIFFGGDPSSVTIFGSSAGAI SVSSLLSPMAGL FHKAIMESGVAIIPYLEAHD 331

QY 271 YEKSEDLQVVAHFCGNNA SDSEALIRCLRTKPSKELLTLSOKTSSFTVVDGAFPPNEPL 330

Db 332 YKSESDQVVAHFCGNNADESEALLKRLTKRPSKELLITTSQTKXSTFRVVDGAFEPNEPL 391  
 QY 331 DLSQKAFKAIPIIIGVNNHECGFLLPMKEAPEILSGNSKSLALHLIQLIHIPOYLHL 390  
 Db 392 DLSQKAFKAIPIIIGVNNHECGFLLPMKEAPEILSGNSKSLALHLIQLIHIPOYLHL 451  
 QY 391 VANEYFHDKSLTEIRDSLLDLDGDFVFPVPAITARYRDGAPYFPEFHRPOCFED 450  
 Db 452 VANEYFHDKSLTEIRDSLLDLDGDFVFPVPAITARYRDGAPYFPEFHRPOCFED 511  
 QY 451 TKPAFYKADHAEVRFVFGAFLKGDIVMEGATEEEKLSRKKMKYVATFARTGNPKN 510  
 Db 512 TKPAFYKADHAEVRFVFGAFLKGDIVMEGATEEEKLSRKKMKYVATFARTGNPKN 571  
 QY 511 DL 512  
 Db 572 DL 573

RESULT 7  
 ABP61006  
 ID ABP61006 strand; protein; 356 AA.  
 AC ABP61006;  
 DT 10-SEP-2002 (first entry)  
 DE Novel human protein. SEQ ID 93.

Human; cytostatic; vulnary; antiarteriosclerotic; antiparkinsonian;  
 neurotropic; neuroprotective; immunosuppressive; haemostatic;  
 antiinflammatory; cardiant; antitumor; virucide; antithyroid;  
 wound healing disorders; atherosclerosis; Parkinson's disease;  
 Alzheimer's disease; autoimmune disorder; haematopoietic disorder;  
 inflammation; neoplastic disease; nervous system disorder;  
 cardiovascular disorders; pancreatitis; respiratory disorder;  
 hyperproliferation; systemic autoimmune disease; hyper-immunity;  
 developmental abnormality; gastrointestinal ulceration; neuropathy;  
 haematological disease; metabolic disease; sperm dysfunction;  
 thyroid disorder; hypothyroidism; brain damage; colitis;  
 cone photo-transduction deficiency; neurological disease; stroke;  
 angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;  
 trachea; thymus; lymph node; muscular system; obesity; anorexia;  
 growth abnormality; precocious puberty.

Homo sapiens.

W0200250105-A1.

27-JUN-2002.

17-DEC-2001; 2001MO-US049232.

19-DEC-2000; 2000US-0256710P.

20-DEC-2000; 2000US-0257048P.

09-JAN-2001; 2001US-0260482P.

30-JAN-2001; 2001US-0264922P.

06-FEB-2001; 2001US-0266797P.

19-MAR-2001; 2001US-0276988P.

04-APR-2001; 2001US-0281535P.

08-MAY-2001; 2001US-0289622P.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PA (GLAXO ) GLAXO GROUP LTD.

PI Agarwal P, Birkeland M, Cogswell JP, Kabnick KF, Lai Y,

PI Marcensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q,

DR WPI, 2002-508784/54.

DR N-PSDB; AB086171.

XX Secreted proteins and polynucleotides useful as vaccines for preventing  
 PT or treating various diseases e.g. cancer, wounds, atherosclerosis,  
 PT Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.  
 XX Claim 1(a); Page 315; 335pp; English.

XX The invention relates to an isolated polypeptide with signal sequences  
 CC which allow it to be secreted extracellularly or membrane associated. The  
 CC activity of polypeptides of the invention may be described as,  
 CC cytostatic, vulnary, antiarteriosclerotic, antiparkinsonian, neurotropic,  
 CC neuroprotective, immunosuppressive, haemostatic, antiinflammatory,  
 CC cardiant, antitumor, virucide, antithyroid, cerebroprotective, anorectic,  
 CC and metabolic. Polypeptides and polynucleotides of the invention are  
 CC useful in the treatment, or as a vaccine in the prevention of, cancer,  
 CC wound healing disorders, infection, atherosclerosis, Parkinson's disease  
 CC and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,  
 CC inflammation, neoplastic diseases, nervous system related disorders and  
 CC cardiovascular disorders, systemic autoimmune disease, hyper-immunity,  
 CC hyperproliferation, hyperproliferation, hyperproliferation,  
 CC developmental abnormality, gastrointestinal ulceration, neuropathy,  
 CC haematological diseases, metabolic diseases, sperm dysfunction, thyroid  
 CC disorders e.g. hypothyroidism, brain damage, colitis, cone photo-  
 CC transduction deficiency, neurological diseases, stroke, angiogenesis,  
 CC ovulation disorders, diseases in the spinal cord, thyroid gland, heart,  
 CC trachea, thymus, lymph node and muscular system, obesity, anorexia,  
 CC growth abnormalities, and alleviation of precocious puberty. The  
 CC sequences given in records ABP60965-ABP61019 represent novel human  
 CC proteins of the invention

SO Sequence 356 AA:

Query Match 58.5%; Score 340; DB 5; Length 356;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 ILSPAKLFLFKAIMESGVAIIPILEAHDKSSDLQVVAHFCGNNADESEALLKRLTKR 301  
 Db 17 ILSPAKLFLFKAIMESGVAIIPILEAHDKSSDLQVVAHFCGNNADESEALLKRLTKR 76  
 QY 302 PSKELLITTSQTKXSTFRVVDGAFEPNEPLDLSQKAFKAIPIIIGVNNHECGFLLPMKEA 361  
 Db 77 PSKELLITTSQTKXSTFRVVDGAFEPNEPLDLSQKAFKAIPIIIGVNNHECGFLLPMKEA 136  
 QY 362 PEILSGNSKSLALHLIQLIHIPOYLHLVANEYFHDKSLTEIRDSLLDLDGDFVFP 421  
 Db 137 PEILSGNSKSLALHLIQLIHIPOYLHLVANEYFHDKSLTEIRDSLLDLDGDFVFP 196  
 QY 422 ALITARYHRDAGAVYFEFRRHRPOCFEDTKPAFYKADHAEVRFVFGAFLKGDIVMEF 481  
 Db 197 ALITARYHRDAGAVYFEFRRHRPOCFEDTKPAFYKADHAEVRFVFGAFLKGDIVMEF 256  
 QY 482 GATEEEKLSRKKMKYVATFARTGNPKNGLSLMPAVNLTBOYLQDLNMSGQRLKEPR 541  
 Db 257 GATEEEKLSRKKMKYVATFARTGNPKNGLSLMPAVNLTBOYLQDLNMSGQRLKEPR 316  
 QY 542 VDFWTSITPILISASDMLHSPSSLTFLSLQFFFFCAP 581  
 Db 317 VDFWTSITPILISASDMLHSPSSLTFLSLQFFFFCAP 356

RESULT 8

ID ADB64065 standard; protein; 469 AA.

XX ADB64065;

DT 04-DEC-2003 (first entry)

DE Human protein encoded by clone BRAWH20021910.

XX Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;

XX cell regeneration; membrane protein; signal transduction-related protein;



KW transcription-related protein; osteoporosis; neurological disease;  
 KW cancer; tumour.  
 OS Homo sapiens.  
 XX EPI308459-A2.  
 FN  
 XX  
 PD 07-MAY-2003.  
 XX  
 XX 28-MAR-2002; 2002EP-00007401.  
 PR  
 XX 05-NOV-2001; 2001JP-00379298.  
 PR 25-JAN-2002; 2002US-00350978.  
 PA (HELI-) HELIX RES INST.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 XX  
 XX Isegai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,  
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,  
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
 XX  
 DR WPI; 2003-450961/43.  
 DR N-PSDB; ADB62095.  
 XX  
 PT New polynucleotides and polypeptides, useful for developing a diagnostic  
 PT marker or medicines for regulation of their expression and activity, or  
 PT as targets of gene therapy.  
 XX  
 XX Claim 1; Page: 222pp; English.  
 XX  
 CC The invention discloses a polynucleotide comprising a sequence selected  
 CC from 1970 fully defined nucleotide sequences which encode novel  
 CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide  
 CC or its partial peptide, an antibody binding to the polypeptide or peptide  
 CC of the polynucleotide, immunologically assaying the polypeptide or  
 CC peptide of the polynucleotide by contacting the polypeptide or peptide  
 CC with the antibody of the encoded protein, and observing the binding  
 CC between the two, a transformant carrying the polynucleotide in an  
 CC expressible manner and an antisense polynucleotide. The oligonucleotide  
 CC is useful as a primer for synthesising the polynucleotide, or as a probe  
 CC for detecting the polynucleotide. The polynucleotides and encoded  
 CC proteins are useful as pharmaceutical agents and many disease-related  
 CC genes may be included in them, for developing a diagnostic marker or  
 CC medicines for regulation of their expression and activity, or as targets  
 CC of gene therapy. The genes are involved in tissue and/or cell  
 CC regeneration. Membrane proteins, signal transduction-related proteins,  
 CC transcription-related proteins, disease-related proteins and genes  
 CC encoding them can be used as indicators for diseases (e.g. osteoporosis,  
 CC neurological diseases, cancer, tumours. The cDNA may be used to regulate  
 CC the activity or expression of the encoded protein to treat diseases. The  
 CC sequence presented is a protein of the invention. Note: Some of the  
 CC sequence data for this patent is not represented in the printed  
 CC specification, but is based on sequence information supplied by the  
 CC European Patent Office.  
 CC  
 XX  
 XX Sequence 469 AA;  
 SQ  
 Query Match 56.6%; Score 329; DB 7; Length 469;  
 Best Local Similarity 99.8%; Pred. No. 8-5e-313;  
 Matches 429; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 113 MKKHYPRKGVSEDCLYNTIYVPAHADGSKLPVLVMPFGAFKTSASIFGSLAAVE 172  
 DB 1 MKKHYPRKGVSEDCLYNTIYVPAHADGSKLPVLVMPFGAFKTSASIFGSLAAVE 60  
 QY 173 DVLVVVVVRLGIFGFFTTWDQAHAPGNMAFKDQVALSWVQKNIFFGGDPSSVTIFGSS 232  
 DB 61 DVLVVVVVRLGIFGFFTTWDQAHAPGNMAFKDQVALSWVQKNIFFGGDPSSVTIFGSS 120  
 QY 223 AGAIVSSIIISLSPMAKGLFHKAIMSGVAIIPLYLAHDYKESDIOVVAHFQGNNAOSDE 292  
 DB 121 AGAIVSSIIISLSPMAKGLFHKAIMSGVAIIPLYLAHDYKESDIOVVAHFQGNNAOSDE 180

QY 293 ALNCLRTKPSKELLTTSQTKTSFTRVVDGAFPNNEBLDLSOKAFKAIPSIIGVNNHEC 352  
 DB 181 ALNCLRTKPSKELLTTSQTKTSFTRVVDGAFPNNEBLDLSOKAFKAIPSIIGVNNHEC 240  
 QY 353 GFLPMEKAPETLSGNSKSLALHLIONIHLIPPOYLHLVANEYFHDGSLTEIRDSLLDL 412  
 DB 241 GFLPMEKAPETLSGNSKSLALHLIONIHLIPPOYLHLVANEYFHDGSLTEIRDSLLDL 300  
 QY 413 LGDVFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKRAFYKADHAEVRFVFGAF 472  
 DB 301 LGDVFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKRAFYKADHAEVRFVFGAF 360  
 QY 473 LKGDIVMEGATEEBSKLSRMMKMYATTFPARTGNPNNDLSLWPAHYLLEQYLDLIMS 532  
 DB 361 LKGDIVMEGATEEBSKLSRMMKMYATTFPARTGNPNNDLSLWPAHYLLEQYLDLIMS 420  
 QY 533 LGORLKEPRV 542  
 DB 421 LGORLKEPRV 430  
 RESULT 9  
 ABP61005  
 ID ABP61005 standard; protein; 581 AA.  
 AC  
 AC ABP61005;  
 DT 10-SEP-2002 (first entry)  
 XX  
 DE Novel human protein. SEQ ID 92.  
 XX  
 KW Human; cytosolic; vulnery; antiarteriosclerotic; antiparkinsonian;  
 KW nootropic; neuroprotective; immunosuppressive; haemostatic;  
 KW antiinflammatory; cardiac; antilucer; virucide; antithyroid;  
 KW cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;  
 KW wound healing disorder; atherosclerosis; Parkinson's disease;  
 KW Alzheimer's disease; autoimmune disorder; haematopoietic disorder;  
 KW inflammation; neoplastic disease; nervous system disorder;  
 KW cardiovascular disorders; pancreatic; respiratory disorder;  
 KW hyperproliferation; systemic autoimmune disease; hyper-immunity;  
 KW developmental abnormality; gastrointestinal ulceration; neuropathy;  
 KW haematological disease; metabolic disease; sperm dysfunction;  
 KW thyroid disorder; hypothyroidism; brain damage; colitis;  
 KW cone photo- transduction deficiency; neurological disease; stroke;  
 KW tracheas; chymus; lymph node; muscular system; obesity; anorexia;  
 KW growth. abnormality; precocious puberty.  
 KW  
 OS Homo sapiens.  
 XX  
 XX MO200250105-A1.  
 XX  
 XX 27-JUN-2002.  
 PD  
 XX  
 XX 17-DEC-2001; 2001WO-US049232.  
 PF  
 XX  
 PR 19-DEC-2000; 2000US-0256710P.  
 PR 20-DEC-2000; 2000US-0257048P.  
 PR 09-JAN-2001; 2001US-0260482P.  
 PR 30-JAN-2001; 2001US-0264922P.  
 PR 06-FEB-2001; 2001US-0266797P.  
 PR 19-MAR-2001; 2001US-0276988P.  
 PR 04-APR-2001; 2001US-0281535P.  
 PR 08-MAY-2001; 2001US-0286622P.  
 XX  
 XX (SMK) SMITHLINE BEECHAM CORP.  
 PA (SMK) SMITHLINE BEECHAM PLC.  
 PA (GLAX) GLAXO GROUP LTD.  
 XX  
 PI Agarwal P, Birkeland M, Cogswell JP, Kabinick KF, Lai Y;  
 PI Matensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q;  
 XX WPI; 2002-508784/54.

DR N-PSDB; ABQ68170.  
XX  
PT Secreted proteins and polynucleotides useful as vaccines for preventing  
PT or treating various diseases e.g. cancer, wounds, atherosclerosis,  
PT Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.  
XX  
XX Claim 1(a); Page 313-314; 335pp; English.  
CC The invention relates to an isolated polypeptide with signal sequences  
CC which allow it to be secreted extracellularly or membrane associated. The  
CC activity of polypeptides of the invention may be described as,  
CC cytotoxic, vulnery, antiarteriosclerotic, antiparkinsonian, nocrotropic,  
CC neuroprotective, immunosuppressive, haemostatic, antiinflammatory,  
CC cardiant, antitumor, vincristine, antithyroid, cerebroprotective, anorectic,  
CC and metabolic. Polypeptides and polynucleotides of the invention are  
CC useful in the treatment, or as a vaccine in the prevention of, cancer,  
CC wound healing disorders, infection, atherosclerosis, Parkinson's disease  
CC and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,  
CC inflammation, neoplastic diseases, nervous system related disorders and  
CC cardiovascular disorders, pancreatitis, respiratory disorder.  
CC hyperproliferation, systemic autoimmune disease, hyper-immunity,  
CC developmental abnormality, gastrointestinal ulceration, neuropathy,  
CC haematological diseases, metabolic diseases, sperm dysfunction, thyroid  
CC disorders e.g. hypothyroidism, brain damages, colitis, cone photo-  
CC transduction deficiency, neurological diseases, stroke, angiogenesis,  
CC ovulation disorders, diseases in the spinal cord, thyroid gland, heart,  
CC trachea, thymus, lymph node and muscular system, obesity, anorexia,  
CC growth abnormalities, and alleviation of precocious puberty. The  
CC sequences given in records ABP0965-ABP61019 represent novel human  
CC proteins of the invention  
XX  
SQ Sequence 581 AA;  
Query Match 56.5%; Score 328; DB 5; Length 581;  
Best Local Similarity 100.0%; Pred. No. 9.9e-312;  
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 31 GPSAEGPQNRRLTMIGQKQVTVLGSPPVAVFLGVPFAAPPLGSLRFTNPOAPSPMDNL 90  
Db 25 GPSAEGPQNRRLTMIGQKQVTVLGSPPVAVFLGVPFAAPPLGSLRFTNPOAPSPMDNL 84  
OY 91 REATSYPLCLQNSEWMLLDQHMLKVHPKFGVSEDCLYNTYAPAHADTGSRLPYLWVF 150  
Db 85 REATSYPLCLQNSEWMLLDQHMLKVHPKFGVSEDCLYNTYAPAHADTGSRLPYLWVF 144  
OY 151 PGAFKTSASIFDGSALAAVEDLVVVVYVYRGLGIFGFTTMOOHAGNNAFDDVAAIS 210  
Db 145 PGAFKTSASIFDGSALAAVEDLVVVVYVYRGLGIFGFTTMOOHAGNNAFDDVAAIS 204  
OY 211 WVGKNIEFGGDPSSVTTFESAGAISVSSLLISPAKGLFHKAINESGVAIIPYLEAHD 270  
Db 205 WVGKNIEFGGDPSSVTTFESAGAISVSSLLISPAKGLFHKAINESGVAIIPYLEAHD 264  
OY 271 YKSESDQVVAHFCGNNADESEALLRLRTPKSKELLTTSQTKSTRVVDGAFPPNEPL 330  
Db 265 YKSESDQVVAHFCGNNADESEALLRLRTPKSKELLTTSQTKSTRVVDGAFPPNEPL 324  
OY 331 DLISQKAFKAIPIISIGVNNHBCGFLPLPM 358  
Db 325 DLISQKAFKAIPIISIGVNNHBCGFLPLPM 352  
RESULT 10  
ABU54639  
ID ABU54639 standard; protein; 581 AA.  
XX  
XX ABU54639;  
AC  
XX  
XX 03-JUN-2003 (first entry)  
DT  
XX  
XX Human NOVX polypeptide #98.  
DE  
XX  
XX Human; NOVX; metabolic disorder; cardiomyopathy; diabetes; ASD;

KW hypertension; congenital heart defect; aortic stenosis; valve disease;  
KW atrial septal defect; atriocentricular canal defect; ductus arteriosus;  
KW pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD;  
KW tuberculous sclerosis; scleroderma; atherosclerosis; infectious disease;  
KW obesity; anorexia; neurodegenerative disorder; Alzheimer's disease;  
KW Parkinson's disease; immune disorder; haematopoietic disorder;  
KW haemophilia; hypercoagulation; Crohn's disease; cancer.  
XX  
XX Homo sapiens.  
XX  
XX WO200281498-A2.  
XX  
XX 17-OCT-2002.  
XX  
XX 03-APR-2002; 2002MC-US010780.  
XX  
XX 03-APR-2001; 2001US-0281086P.  
XX 03-APR-2001; 2001US-0281136P.  
XX 05-APR-2001; 2001US-0281863P.  
XX 05-APR-2001; 2001US-0281906P.  
XX 06-APR-2001; 2001US-0282020P.  
XX 10-APR-2001; 2001US-0282930P.  
XX 10-APR-2001; 2001US-0282934P.  
XX 12-APR-2001; 2001US-0283512P.  
XX 13-APR-2001; 2001US-0283710P.  
XX 17-APR-2001; 2001US-0284234P.  
XX 19-APR-2001; 2001US-0285325P.  
XX 20-APR-2001; 2001US-0285381P.  
XX 20-APR-2001; 2001US-0285609P.  
XX 23-APR-2001; 2001US-0285748P.  
XX 23-APR-2001; 2001US-0285890P.  
XX 24-APR-2001; 2001US-0286068P.  
XX 25-APR-2001; 2001US-0286292P.  
XX 27-APR-2001; 2001US-0287213P.  
XX 02-MAY-2001; 2001US-0288257P.  
XX 29-MAY-2001; 2001US-0294164P.  
XX 30-MAY-2001; 2001US-0294484P.  
XX 18-JUN-2001; 2001US-0298952P.  
XX 19-JUN-2001; 2001US-0299237P.  
XX 19-JUN-2001; 2001US-0299276P.  
XX 12-SEP-2001; 2001US-0318750P.  
XX 25-SEP-2001; 2001US-0324800P.  
XX 25-SEP-2001; 2001US-0324802P.  
XX 27-SEP-2001; 2001US-0325684P.  
XX 17-OCT-2001; 2001US-0330143P.  
XX 14-NOV-2001; 2001US-0332131P.  
XX 14-NOV-2001; 2001US-0332240P.  
XX 14-NOV-2001; 2001US-0332799P.  
XX 21-NOV-2001; 2001US-0332115P.  
XX 04-DEC-2001; 2001US-0337621P.  
XX 03-JAN-2002; 2002US-0345783P.  
XX 16-JAN-2002; 2002US-0350251P.  
XX 02-APR-2002; 2002US-00114270.  
(CURA-) CURAGEN CORP.  
XX  
XX Guo X, Kekuda R, Miller CE, Malyankar UM, Szytek KA;  
PI Paturajan W, Liu X, Gusev VV, Li L, Vernet CAM, Zernusen BD;  
PI Gorman L, Shenoy SG, Pena CE, Smithson G, Burgess CE, Gerlach V;  
PI Padigaru M, Shimkets RA, Gangoli BA, Taupier RJ, Caeman SJ, Ji W;  
PI Anderson DW, Leite MW, Raetelli L, Edinger SR, Stone DJ;  
PI MacDougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA;  
PI Ellerman K;  
XX  
XX WPI; 2003-046858/04.  
XX  
XX N-PSDB; ABX72267.  
XX  
XX  
XX New isolated NOVX polypeptide useful for treating atherosclerosis,  
XX metabolic disorders, diabetes, obesity, infectious disease, anorexia,  
XX neurodegenerative disorders, Alzheimer's disease and cancer.  
XX  
XX Claim 1; Page 303; 666pp; English.



The invention relates to human polypeptides, termed NOVX, and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for diagnosing disease, and screening for potential therapeutic agents. The sequences are useful for treating metabolic disorders, cardiovascularity, diabetes, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atriocentricular canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberculous scleritis, scleroderma, atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease and cancer. Sequences ABUS4542-ABUS4647 represent human NOVX polypeptides of the invention

**SQ Sequence 581 AA;**

Query Match	56.5%	Score 328	DB 6	Length 581
Best Local Similarity	100.0%	Pred. No.	9	9e-312
Matches 328	Conservative 0	Mismatches 0	Gaps 0	

Qy	33	GSBAEPQNTLRLGMIOGKQVTVLDS	PPVNVVFLGVPAAAPLGLSLFTTNPQPAS	PMNDL	90	
Db	27	GSBAEPQNTLRLGMIOGKQVTVLDS	PPVNVVFLGVPAAAPLGLSLFTTNPQPAS	PMNDL	86	
Qy	91	REATSYPNLCLONSEWMLLDQHM	LKVHYPKGVSEDCIYINITYAPAHADTGS	KLPVLWVF	150	
Db	87	REATSYPNLCLONSEWMLLDQHM	LKVHYPKGVSEDCIYINITYAPAHADTGS	KLPVLWVF	146	
Qy	151	PGGAFKTSASIFDGSALAAVEDVL	VVVVQYRLGIFGFFTTMDQHPANNAFKDQV	AAALS	210	
Db	147	PGGAFKTSASIFDGSALAAVEDVL	VVVVQYRLGIFGFFTTMDQHPANNAFKDQV	AAALS	206	
Qy	211	WQOKNIEFGDPSSVYTFGESSAGAI	SVSSLLSPMAKGLFHAKIMESGVALI	PYLEARD	270	
Db	207	WQOKNIEFGDPSSVYTFGESSAGAI	SVSSLLSPMAKGLFHAKIMESGVALI	PYLEARD	266	
Qy	271	YKESSELDQVNAHPCGNNASDSE	ALLRLCRLTRPSKELLTL	LSQKTSFTRVVDGAF	FFPNEPL	330
Db	267	YKESSELDQVNAHPCGNNASDSE	ALLRLCRLTRPSKELLTL	LSQKTSFTRVVDGAF	FFPNEPL	326
Qy	331	DLLSQAKAFKAIPSIITGVNNH	CEGFLPLPM	358		
Db	327	DLLSQAKAFKAIPSIITGVNNH	CEGFLPLPM	354		

## RESULT 11

**ID** ADR19663 standard; protein; 618 AA.

AC	ADR19663;
XX	
DT	07-OCT-2004 (first entry)

KM	drug-metabolizing enzyme; DME; cytostatic; immunosuppressive;
KM	antiinflammatory; endocrine; pathological; gastrointestinal;
KM	hepatotropic; cancer; cell proliferative disorder; autoimmune disorder
KM	inflammatory disorder; endocrine disorder; eye disorder;
KM	gastrointestinal disorder; liver disorder; metabolic disorder; enzyme;
KM	human.

**OS Homo sapiens.**

PN WO200226988-A2

PD 04-APR-2002

PR 28-SEP-2001; 2001WO-US030662.

PR 29-SEP-2000; 2000US-0236947P

PR 20-OCT-2000; 2000US-0242323P.

PR 20-OCT-2000; 2000US-0242323P.

PR 09-NOV-2000; 2000US-0247581P.  
PR 16-NOV-2000; 2000US-0249519P.  
PR 22-NOV-2000; 2000US-0252834P.  
PR 30-NOV-2000; 2000US-0250567P.  
XX  
XX  
PA (INCY-) INCYTE GENOMICS INC.

PA (INCY-) INCYTE GENOMICS INC.

PI Aizawai Y, Baughn AR, Borowsky ML, Ding L, Duggan BM; Khan FA,  
PI Elliott VS, Gandhi AR, Giffen JA, Hafala AJA, Ison CH,  
PI Lal P, Lee BA, Lu DAM, Nguyen DB, Arvizu C, Policky JL, Ramkumar J,  
PI Ring HZ, Sandanwala MS, Tang YT, Tribouley CM, Nairinder WK;  
PI Welsh RT, Warren BA, Xu Y, Yang J, Yao MG, Yue H;

DR WPI; 2002-362498/39.

DR N-PSDB; ADRL 9681.

PT Human drug metabolizing enzymes, useful in the diagnosis and treatment of  
PT disorders associated with aberrant (DME) activity, e.g., cancer and  
PT autoimmune disorders.

PS Claim 1; SEQ ID NO 2; 142pp; English

CC This invention relates to novel drug metabolising enzymes (DME) and the  
CC nucleotide sequences which encode them. The invention may be useful for  
CC the development of compounds with a cytostatic, immunosuppressive,  
CC antiinflammatory, endocrine, ophthalmological, gastrointestinal or  
CC hepatotropic activity acting as an agonist or antagonist of drug  
CC metabolising enzyme activity. The invention may be used in the diagnosis  
CC and treatment of disorders associated with decreased or increased  
CC expression or activity of drug metabolising enzymes. Such disorders  
CC include cancer, cell proliferative disorders, autoimmune/inflammatory,  
CC endocrine, eye, gastrointestinal (including liver disorders) and  
CC metabolic disorders. The present sequence is that of a human drug  
CC metabolising enzyme (DME) of the invention. Note: This sequence did not  
CC form part of the printed specification but was obtained in electronic  
CC format from EPO.

**SQ Sequence 618 AA:**

```
Query Match      56.5%; Score 328; DB 5; length 618;
Best Local Similarity 100.0%; Pred. No. 1,1e-311;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

Qy	31	GSABSPQNTLGMIOGQVTVGSPVAVVFLGVPPAAPPLGSLRTNQPASPMNDL	90
Db	92	GSABSPQNTLGMIOGQVTVGSPVAVVFLGVPPAAPPLGSLRTNQPASPMNDL	15
Qy	91	REATSPVNLCLNSEMLLDQMLKVHPKFGVSEDCLYLNIYAPAHADTSKLPVLVWF	156
Db	152	REATSPVNLCLNSEMLLDQMLKVHPKFGVSEDCLYLNIYAPAHADTSKLPVLVWF	211
Qy	151	PGGAFYTGASIFDSSALAAVEDLVVVVQYRLGIFGFTTMDQAHAPNMAFKQVVALS	210
Db	212	PGGAFYTGASIFDSSALAAVEDLVVVVQYRLGIFGFTTMDQAHAPNMAFKQVVALS	273
Qy	211	WYQKNIFFPGDPSSVTIFGESAGAIYSVSLISPMAGLPHKAIMESGVALIPLYEAMD	276
Db	272	WYQKNIFFPGDPSSVTIFGESAGAIYSVSLISPMAGLPHKAIMESGVALIPLYEAMD	333
Qy	271	YKXSEDLQVVAHFCGNNASDSEALIRCIKRTYPSKELLTLSQKTSFTRVVDGAFPPNEPL	330
Db	332	YKXSEDLQVVAHFCGNNASDSEALIRCIKRTYPSKELLTLSQKTSFTRVVDGAFPPNEPL	393
Qy	331	DLLSQAKFKAIPSIIGVNNHECGFLPMP	358
Db	392	DLLSQAKFKAIPSIIGVNNHECGFLPMP	419

## RESULT 12

ID ADC55524 standard; protein; 224 AA

AC ADC55524



XX 06-NOV-2001 (first entry)  
XX Human polypeptide SEQ ID NO 19709.  
DE  
XX  
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
XX tissue growth factor; stem cell growth factor; haematopoiesis;  
XX tissue growth factor; immunomodulatory; cancer; leukaemia;  
XX nervous system disorders; arthritis; inflammation.  
OS Homo sapiens.  
XX  
XX WO200164835-A2.  
XX  
XX 07-SEP-2001.  
XX  
XX 26-FEB-2001; 2001WO-US004927.  
XX  
XX 28-FEB-2000; 2000US-00515126.  
XX 18-MAY-2000; 2000US-00577409.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Dermanac RT;  
XX  
XX MPI; 2001-514838/56.  
XX  
XX N-PSDB; AA185748.  
XX  
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing  
XX and treating e.g. leukemia, inflammation and immune disorders.  
XX  
XX Claim 20; SEQ ID NO 19709; 1399bp + Sequence listing; English.  
XX  
XX The invention relates to human polynucleotides (AA179941-AA193841) and  
XX the encoded proteins (AA000010-AA013910) that exhibit activity elating to  
XX cytokine, cell proliferation or cell differentiation or which may induce  
XX production of other cytokines in other cell populations. The  
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or  
XX peptide therapy. The polypeptides have various cytokine-like activities,  
XX e.g. stem cell growth factor activity, haematopoiesis regulating  
XX activity, tissue growth factor activity, immunomodulatory activity and  
XX activin/inhibin activity and may be useful in the diagnosis and/or  
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and  
XX inflammation. Note: The sequence data for this patent did not form part  
XX of the printed specification, but was obtained in electronic format  
XX directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 124 AA;  
SQ  
Query Match 9.5%; Score 55; DB 4; Length 124;  
Best Local Similarity 100.0%; Pred. No. 4.7e-45;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 449 EDTKPAFYKADHDEVRFVFGAFLKGDIVMEFGATEEBKLSRQMKYMATFAR 503  
DB 20 EDTKPAFYKADHDEVRFVFGAFLKGDIVMEFGATEEBKLSRQMKYMATFAR 74  
RESULT 15  
ID AAE20909  
AAE20909 standard; protein; 306 AA.  
XX  
XX AAE20909;  
XX  
XX 01-JUL-2002 (first entry)  
XX  
XX Human carboxylesterase-like enzyme protein #1.  
DE  
XX Human; carboxylesterase-like enzyme; organophosphorus intoxication;  
XX osteoporosis; gene therapy; osteoporosis; antisense therapy; cytostatic;  
XX detoxifying agent; Paget's disease; bone implant degradation; cancer;  
XX dental implant; enzyme; gene expression.  
XX

OS Homo sapiens.  
XX  
XX WO200206454-A2.  
XX  
XX 24-JAN-2002.  
XX  
XX 10-JUL-2001; 2001WO-EP007919.  
XX  
XX 17-JUL-2000; 2000US-0218564P.  
XX  
XX (FARB ) BAYER AG.  
XX  
XX Xiao Y;  
XX  
XX MPI; 2002-195808/25.  
XX  
XX N-PSDB; AAD33344.  
XX  
XX Novel human carboxylesterase-like enzyme polypeptide, regulators of which  
XX are useful for preventing and treating organophosphorus intoxication,  
XX cancer and osteoporosis.  
XX  
XX Claim 25; Fig 5; 92bp; English.  
XX  
XX The invention relates to a purified human carboxylesterase-like enzyme  
XX polypeptide. Carboxylesterase-like enzyme and its DNA are useful for  
XX screening for agents which decrease or modulate the activity of  
XX carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme is  
XX useful for treating a carboxylesterase-like enzyme dysfunction related  
XX disease, such as organophosphorus intoxication, cancer and osteoporosis.  
XX Compounds that increase the ability of human carboxylesterase-like enzyme  
XX to bind to organophosphorus compounds are useful as detoxifying agents.  
XX Carboxylesterase-like enzyme agonists and antagonists are useful for  
XX treating osteoporosis, Paget's disease and degradation of bone implants,  
XX particularly dental implants. Carboxylesterase-like enzyme is useful in  
XX diagnostic assays for detecting diseases and abnormalities or  
XX susceptibility to diseases or abnormalities which encode the enzyme. The  
XX coding sequence of carboxylesterase-like enzyme polynucleotide is useful  
XX in gene therapy and for generating antisense oligonucleotides or  
XX ribozymes which specifically bind to mRNA transcribed from  
XX carboxylesterase-like enzyme DNA. These antisense oligonucleotides are  
XX useful for modulating carboxylesterase-like enzyme gene expression. The  
XX present sequence is human carboxylesterase-like enzyme protein  
XX  
XX Sequence 306 AA;  
SQ  
Query Match 9.3%; Score 54; DB 5; Length 306;  
Best Local Similarity 100.0%; Pred. No. 1e-43;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 179 VOYRLGIGFPTTDDHAGNMAFDOVAALSWQXNIEFGDPSVTIRGES 232  
DB 53 VOYRLGIGFPTTDDHAGNMAFDOVAALSWQXNIEFGDPSVTIRGES 106  
RESULT 16  
ID ABG66757  
ABG66757 standard; protein; 84 AA.  
XX  
XX ABG66757;  
XX  
XX 30-AUG-2002 (first entry)  
XX  
XX Human novel polypeptide #92.  
DE  
XX Human; inflammatory condition; shock; sepsis; immune response; cancer;  
XX wound healing; central nervous system disease; haematopoiesis;  
XX peripheral nervous system disease; amyotrophic lateral sclerosis; tendon;  
XX myofibril cell disorder; lymphoid cell disorder; platelet disorder; bone;  
XX cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;  
XX bone degenerative disorder; periodontal disease; reperfusion injury;  
XX lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection;  
XX allergic condition; thrombolysis; thrombosis; coagulation disorder;  
XX

KW fungal infection.  
XX  
OS Homo sapiens.  
XX  
PN MO200244340-A2.  
XX  
PD 06-JUN-2002.  
XX  
PF 30-NOV-2001; 2001MO-US047004.  
XX  
PR 30-NOV-2000; 2000US-00728952.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YF, Goodrich RM, Liu C, Zhou P, Asundi V, Wang J, Wang D,  
PI Yamazaki V, Ujwal ML, Drmanac RT;  
XX WPI, 2002-508509/54.  
DR N-PSDB; ABR94981.  
XX  
XX Novel nucleic acids and polypeptides for diagnosis, treatment of  
PT inflammatory, autoimmune, nervous system, myeloid or lymphoid cell  
PT disorders, cancer and promoting wound healing.  
XX  
PS Claim 10; Page 672; 672pp; English.  
XX  
CC The invention relates to human novel polynucleotides and associated  
CC polypeptides. The polynucleotides and polypeptides are useful for  
CC treating inflammatory conditions such as arthritis, nephritis, Crohn's  
CC disease, ischaemia-reperfusion injury, shock, sepsis, immune responses  
CC and cancer and for promoting wound healing. The sequences are used to  
CC induce the proliferation of neural cells and regeneration of nerve and  
CC brain tissue, and are useful for the treatment of central and peripheral  
CC nervous system diseases and neuropathies, such as Alzheimer's disease,  
CC Parkinson's disease, Huntington's disease and amyotrophic lateral  
CC sclerosis. The sequences are involved in chemotactic or chemokinetic  
CC activity, regulation of hematopoiesis, treatment of myeloid or lymphoid  
CC cell disorders and platelet disorders such as thrombocytopenia,  
CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue  
CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of  
CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal  
CC disease. The sequences of the invention are also useful for gut  
CC protection or regeneration and treatment of lung or liver fibrosis,  
CC reperfusion injury in various tissues, immune deficiencies and disorders  
CC including severe combined immunodeficiency (SCID), bacterial or fungal  
CC infections, autoimmune disorders e.g. multiple sclerosis and myasthenia  
CC gravis, allergic conditions such as asthma, thrombolytic or thrombotic  
CC and coagulation disorders. Sequences ABR66666-ABR66758 represent human  
CC novel polypeptides of the invention  
XX  
SQ Sequence 84 AA;  
Query Match 8.8%; Score 51; DB 5; Length 84;  
Best Local Similarity 100.0%; Pred. No. 2.7e-41;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 179 VQYRLGIFGFTTWDQHPGNNAFKDQVALSWQXNIIEFGDPSSVTIF 229  
DB 6 VQYRLGIFGFTTWDQHPGNNAFKDQVALSWQXNIIEFGDPSSVTIF 56  
RESULT 17  
AAM16665  
ID AAM16665 standard; protein; 49 AA.  
XX  
AC AAM16665;  
XX  
DT 12-OCT-2001 (first entry)  
XX  
DE Peptide #3099 encoded by probe for measuring cervical gene expression.  
XX Probe; human; microarray; gene expression; cervical epithelial cell;  
KW cervical cancer.

XX  
OS Homo sapiens.  
XX  
PN MO200157278-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001MO-US000670.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
XX  
PR 30-JUN-2000; 2000US-00608408.  
XX  
PR 03-AUG-2000; 2000US-00632366.  
XX  
PR 21-SEP-2000; 2000US-0234687P.  
XX  
PR 27-SEP-2000; 2000US-0236359P.  
XX  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
PI WPI, 2001-488901/53.  
XX  
DR WPI, 2001-488901/53.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human cervical epithelial cells.  
XX  
PS Claim 27; SEQ ID NO 21491; 487pp; English.  
XX  
CC The present invention relates to human single exon nucleic acid probes  
CC (SENPs: see A110068-A1128459). The present sequence is a peptide encoded  
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs  
CC can be used to produce a single exon microarray, which can be used for  
CC measuring human gene expression in a sample derived from human cervical  
CC epithelial cells. By measuring gene expression, the probes are therefore  
CC useful in grading and/or staging of diseases of the cervix, notably  
CC cervical cancer. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at [http://pub.wipo.int/published\\_pct\\_sequences](http://pub.wipo.int/published_pct_sequences)  
XX  
SQ Sequence 49 AA;  
Query Match 8.4%; Score 49; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.5e-39;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 432 AGAPVYFEYEFRRPQCEEDTTPAFVKADHDEVRFVFGAFLKGDIVMF 480  
DB 1 AGAPVYFEYEFRRPQCEEDTTPAFVKADHDEVRFVFGAFLKGDIVMF 49  
RESULT 18  
ABR35649  
ID ABR35649 standard; peptide; 49 AA.  
XX  
AC ABR35649;  
XX  
DT 04-FEB-2002 (first entry)  
XX  
DE Peptide #3155 encoded by human foetal liver single exon probe.  
XX  
XX Human; foetal liver; gene expression; single exon nucleic acid probe.  
XX  
OS Homo sapiens.  
XX  
PN MO200157277-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001MO-US000669.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
XX  
PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-483447/52.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human fetal liver.  
XX  
PS Claim 27; SEQ ID NO 28284; 639pp + Sequence Listing; English.  
XX  
CC The invention relates to a single exon nucleic acid probe for measuring  
CC human gene expression in a sample derived from human foetal liver. The  
CC single exon nucleic acid probes may be used for predicting, measuring and  
CC displaying gene expression in samples derived from human fetal liver. The  
CC present sequence is a peptide encoded by a single exon nucleic acid probe  
CC of the invention. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 49 AA;

Query Match 8.4%; Score 49; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.5e-39;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 432 AGAIVYEFERHRRPQCEDTTPAFVKADHAEVRFVFGAFLKGDIVMF 480  
DB 1 AGAIVYEFERHRRPQCEDTTPAFVKADHAEVRFVFGAFLKGDIVMF 49

RESULT 19  
ID AAM29149 standard; protein; 49 AA.  
XX  
AC AAM29149;  
XX  
DT 17-OCT-2001 (first entry)  
XX  
DE Peptide #1186 encoded by probe for measuring placental gene expression.  
XX  
KW Probe; microarray; human; placenta; antenatal diagnosis;  
XX  
KV genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200157272-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000663.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
XX  
PR 30-JUN-2000; 2000US-00608408.  
XX  
PR 03-AUG-2000; 2000US-00632366.  
XX  
PR 21-SEP-2000; 2000US-0234687P.  
XX  
PR 27-SEP-2000; 2000US-0236359P.  
XX  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488897/53.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human placenta.

XX  
XX Claim 27; SEQ ID NO 29418; 654pp; English.  
XX  
PS  
XX  
CC The present invention relates to single exon nucleic acid probes (SENP:  
CC see A13315-A157546). The present sequence is a peptide encoded by one  
CC such probe. The probes are useful for producing a microarray for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from human placenta. The probes are useful for antenatal diagnosis of  
CC human genetic disorders  
XX  
SQ Sequence 49 AA;

Query Match 8.4%; Score 49; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.5e-39;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 432 AGAIVYEFERHRRPQCEDTTPAFVKADHAEVRFVFGAFLKGDIVMF 480  
DB 1 AGAIVYEFERHRRPQCEDTTPAFVKADHAEVRFVFGAFLKGDIVMF 49

RESULT 20  
ID ABB30482 standard; peptide; 49 AA.  
XX  
AC ABB30482;  
XX  
DT 01-FEB-2002 (first entry)  
XX  
DE Peptide #1133 encoded by breast cell single exon nucleic acid probe.  
XX  
KW Human; microarray; single exon probe; gene expression; breast; disease;  
XX  
KV cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200157271-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000662.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
XX  
PR 30-JUN-2000; 2000US-00608408.  
XX  
PR 03-AUG-2000; 2000US-00632366.  
XX  
PR 21-SEP-2000; 2000US-0234687P.  
XX  
PR 27-SEP-2000; 2000US-0236359P.  
XX  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-496933/54.  
XX  
PT New spatially-addressable set of single exon nucleic acid probes, useful  
PT for measuring gene expression in sample derived from human breast,  
PT comprises number of single exon nucleic acid probes.  
XX  
PS Claim 27; SEQ ID NO 13450; 327pp + Sequence Listing; English.  
XX  
CC The invention relates to a spatially-addressable set of single exon  
CC nucleic acid probes for measuring gene expression in a sample derived  
CC from human breast and BT 474 cells. The method involves contacting the  
CC probes with a collection of detectably labeled nucleic acids derived  
CC from mRNA of human breast, and then measuring the label bound to each  
CC probe of the microarray. The probes are useful for verifying the  
CC expression of regions of genomic DNA predicted to encode proteins. They  
CC are useful for gene discovery, and for determining predisposition and/or  
CC prognosing breast disease. Gene expression analysis is useful for  
CC assessing the toxicity of chemical agents on cells. The microarray of  
CC this invention presents a far greater diversity of probes for measuring

CC gene expression, with far less bias than expressed sequence tag  
CC microarrays. The method is suitable for rapid production of functional  
CC information from genomic sequence. The present sequence is a peptide  
CC encoded by a single exon nucleic acid probe of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 49 AA;

Query Match 8.4%; Score 49; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.5e-39;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 AGAPVYFEFRHRPQCFEDTKPAFVKADHDEVRFVFGAFLKGDIVMF 480  
DB 1 AGAPVYFEFRHRPQCFEDTKPAFVKADHDEVRFVFGAFLKGDIVMF 49

RESULT 21

ABB21078  
ID ABB21078 standard; protein; 49 AA.

XX ABB21078;

DT 23-JAN-2002 (first entry)

DE Protein #3077 encoded by probe for measuring heart cell gene expression.

XX Human; gene expression; heart; microarray; vascular system;  
XX cardiovascular disease; hypertension; cardiac arrhythmia;  
XX congenital heart disease.

OS Homo sapiens.

XX WO200157274-A2.

PN 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000666.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

(MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488899/53.

PT Single exon nucleic acid probes for analyzing gene expression in human

PT hearts.

PS Claim 15; SEQ ID NO 22848; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for  
XX measuring human gene expression in a sample derived from human heart (see  
XX ABA21533-ABA41105). The present sequence is a protein encoded by one such  
XX probe. The probes may be used for predicting, measuring and displaying  
XX gene expression in samples derived from the human heart via microarrays.  
XX By measuring gene expression, the probes are useful for predicting,  
XX diagnosing, grading, staging, monitoring and prognosing diseases of the  
XX human heart and vascular system e.g. cardiovascular disease,  
XX hypertension, cardiac arrhythmias and congenital heart disease.  
XX sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences

SEQ Sequence 49 AA;

Query Match 8.4%; Score 49; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.5e-39;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 AGAPVYFEFRHRPQCFEDTKPAFVKADHDEVRFVFGAFLKGDIVMF 480  
DB 1 AGAPVYFEFRHRPQCFEDTKPAFVKADHDEVRFVFGAFLKGDIVMF 49

RESULT 22

AA668842  
ID AAM68842 standard; protein; 49 AA.

XX AAM68842;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 29148.

XX Human; bone marrow expressed exon; gene expression analysis; probe;  
XX microarray; cancer; leukaemia; lymphoma; myeloma.

XX Homo sapiens.

PN WO200157276-A2.

PF 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000668.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

(MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488900/53.

PT Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human bone marrow.

PS Example 4; SEQ ID NO 29148; 658pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid  
XX probes which are derived from genomic sequences expressed in the human  
XX bone marrow. They can be used to measure gene expression in bone marrow  
XX samples, which may enable the improved diagnosis and treatment of cancers  
XX such as lymphoma, leukaemia and myeloma. The present sequence is a  
XX protein encoded by one of the probes of the invention

SEQ Sequence 49 AA;

Query Match 8.4%; Score 49; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.5e-39;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 AGAPVYFEFRHRPQCFEDTKPAFVKADHDEVRFVFGAFLKGDIVMF 480  
DB 1 AGAPVYFEFRHRPQCFEDTKPAFVKADHDEVRFVFGAFLKGDIVMF 49

RESULT 23

AA656465  
ID AAM56465 standard; protein; 49 AA.

AC AAM56465;  
XX  
XX 05-NOV-2001 (first entry)  
DT  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28570.  
XX  
XX Human; brain expressed exon; gene expression analysis; probe: microarray;  
KM Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.  
XX  
XX Homo sapiens.  
OS  
PN WO200157275-A2.  
XX  
PD 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US000667.  
PF  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-483446/52.  
DR  
XX  
XX Single exon nucleic acid probes for analyzing gene expression in human  
PT brains.  
XX  
XX Example 4; SEQ ID NO 28570; 650bp + Sequence Listing; English.  
XX  
XX The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,  
CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
CC epilepsy and cancer. The present sequence is a protein encoded by one of  
CC the probes of the invention  
XX  
XX  
SQ Sequence 49 AA;  
Query Match 8.4%; Score 49; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.5e-39;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 432 AGAPVYFEFRRHRCQCFEDTKPAFYKADHADVRFVFGAFLKGDIVMF 480  
DB 1 AGAPVYFEFRRHRCQCFEDTKPAFYKADHADVRFVFGAFLKGDIVMF 49  
RESULT 24  
ID AAG50502  
ID AAG50502 standard; peptide; 49 AA.  
AC AAG50502;  
XX  
XX 25-FEB-2003 (first entry)  
DT  
XX  
XX Human liver peptide, SEQ ID NO 29150.  
DE  
XX  
XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
KM hypercholesterolaemia; coronary heart disease.  
XX  
XX Homo sapiens.  
OS  
PN WO200157273-A2.  
XX  
PD 09-AUG-2001.

XX  
XX 30-JAN-2001; 2001WO-US000664.  
PF  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-488898/53.  
DR  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human adult liver.  
XX  
XX Claim 27; SEQ ID NO 29150; 658bp; English.  
XX  
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for  
CC measuring human gene expression in a sample derived from human adult  
CC liver, comprising one of 13109 defined nucleotide sequences given in the  
CC specification (or complements/ fragments). The probe hybridises at high  
CC stringency to a nucleic acid molecule expressed in the human adult liver.  
CC (I) may be used for predicting, measuring and displaying gene expression  
CC in samples derived from human adult liver. The genes identified may be  
CC involved in genetic liver diseases such as cirrhosis,  
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
CC associated with coronary heart disease. AAG47348-AAG59930 represent human  
CC liver single exon encoded peptides of the invention. Note: The sequence  
CC information for this patent does not appear in the printed specification  
CC but was obtained in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 49 AA;  
Query Match 8.4%; Score 49; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.5e-39;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 432 AGAPVYFEFRRHRCQCFEDTKPAFYKADHADVRFVFGAFLKGDIVMF 480  
DB 1 AGAPVYFEFRRHRCQCFEDTKPAFYKADHADVRFVFGAFLKGDIVMF 49  
RESULT 25  
ID AAM04381  
ID AAM04381 standard; protein; 49 AA.  
AC AAM04381;  
XX  
XX 09-OCT-2001 (first entry)  
DT  
XX  
XX Peptide #3063 encoded by probe for measuring breast gene expression.  
DE  
XX  
XX Probe; human; breast disease; breast cancer; development disorder;  
KM inflammatory disease; proliferative breast disease; non-carcinoma tumour.  
XX  
XX Homo sapiens.  
OS  
PN WO200157270-A2.  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 29-JAN-2001; 2001WO-US000661.  
PF  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.



21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2002-476286/51.  
 XX  
 PT Novel single exon nucleic acid probe used to measuring gene expression in  
 PT a human breast.  
 XX  
 PS Claim 27; SEQ ID NO 13121; 322pp; English.  
 XX  
 CC The present invention relates to novel single exon nucleic acid probes  
 CC (see A1100010-A110067). The present sequence is a peptide encoded by one  
 CC such probe. The probes are useful for measuring human gene expression in  
 CC a human breast sample, where the probe hybridizes at high stringency to a  
 CC nucleic acid expressed in the human breast. The probes are useful for  
 CC predicting, diagnosing, grading, staging, monitoring and prognosing  
 CC diseases of the human breast, particularly those diseases with polygenic  
 CC inflammatory diseases of the breast, breast cancer, disorders of development,  
 CC breast disease and non-carcinoma tumours. Note: The sequence data for  
 CC this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 49 AA;  
 XX  
 QY  
 Query Match 8.4%; Score 49; DB 4; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-39;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 DB 432 AGAPVYFEFFRRPQCFEDTKPAFYKADHADVRFVFGAFLKGDIVWF 480  
 1 AGAPVYFEFFRRPQCFEDTKPAFYKADHADVRFVFGAFLKGDIVWF 49  
 XX  
 RESULT 26  
 ID ABG38423 standard; peptide; 49 AA.  
 XX  
 AC ABG38423;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 28088.  
 XX  
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200186003-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 30-JAN-2001; 2001MO-US000665.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456E.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.

27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2002-114183/15.  
 XX  
 PT Spatially-addressable set of single exon nucleic acid probes, used to  
 PT measure gene expression in human lung samples.  
 XX  
 PS Claim 27; SEQ ID NO 28088; 634pp; English.  
 XX  
 CC The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of probes  
 CC; the novel set of probes which hybridize at high stringency to a nucleic  
 CC acid expressed in the human lung; measuring gene expression in a sample  
 CC derived from human lung; comprising (a) contacting the array with a  
 CC collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA; and (b) measuring the label detectably bound to each probe of the  
 CC array; identifying exons in a eukaryotic genome, comprising (a)  
 CC algorithmically predicting at least one exon from genomic sequences of  
 CC the eukaryote; and (b) detecting specific hybridization of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarray having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene expression  
 CC analysis, and for identifying exons in a gene, particularly using human  
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
 CC Pudlak syndrome, lymphangioleiomyomatosis, pulmonary haemosiderosis,  
 CC histiocytosis, pulmonary hypertension and hyaline membrane disease. The  
 CC Karsenger syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
 CC present sequence is a peptide/protein encoded by a single exon probe of  
 CC the invention. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 49 AA;  
 XX  
 QY  
 Query Match 8.4%; Score 49; DB 5; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-39;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 DB 432 AGAPVYFEFFRRPQCFEDTKPAFYKADHADVRFVFGAFLKGDIVWF 480  
 1 AGAPVYFEFFRRPQCFEDTKPAFYKADHADVRFVFGAFLKGDIVWF 49  
 XX  
 RESULT 27  
 ID AAE20912 standard; peptide; 41 AA.  
 XX  
 AC AAE20912;  
 XX  
 DT 01-JUL-2002 (first entry)  
 XX  
 DE Carboxylesterase type-B serine peptide #1.



```

XX Carboxylesterase-like enzyme; organophosphorus intoxication; enzyme;
KW osteopathic; gene therapy; osteoporosis; antisense therapy; cytostatic;
KW detoxifying agent; Paget's disease; bone implant degradation; cancer;
KW dental implant; gene expression; carboxylesterase type-B serine.
XX Unidentified.
OS
XX MO200206454-A2.
XX
XX 24-JAN-2002.
XX
XX 10-JUL-2001; 2001WO-EP007919.
XX
XX 17-JUL-2000; 2000US-0218564P.
XX
XX (FARB ) BAYER AG.
XX
XX Xiao Y;
XX
XX WPI, 2002-195808/25.
XX
XX Novel human carboxylesterase-like enzyme polypeptide, regulators of which
XX are useful for preventing and treating organophosphorus intoxication,
XX cancer and osteoporosis.
XX
XX Disclosure; Fig 12; 92pp; English.
XX
XX The invention relates to a purified human carboxylesterase-like enzyme
XX polypeptide. Carboxylesterase-like enzyme and its DNA are useful for
XX screening for agents which decrease or modulate the activity of
XX carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme is
XX useful for treating a carboxylesterase-like enzyme dysfunction related
XX disease, such as organophosphorus intoxication, cancer and osteoporosis.
XX Compounds that increase the ability of human carboxylesterase-like enzyme
XX to bind to organophosphorus compounds are useful as detoxifying agents.
XX Carboxylesterase-like enzyme agonists and antagonists are useful for
XX treating osteoporosis, Paget's disease and degradation of bone implants,
XX particularly dental implants. Carboxylesterase-like enzyme is useful in
XX diagnostic assays for detecting diseases and abnormalities or
XX susceptibility to diseases or abnormalities related to the presence of
XX mutations in the nucleic acid sequences which encode the enzyme. The
XX coding sequence of carboxylesterase-like enzyme polynucleotide is useful
XX in gene therapy and for generating antisense oligonucleotides or
XX ribozymes which specifically bind to mRNA transcribed from
XX carboxylesterase-like enzyme DNA. These antisense oligonucleotides are
XX useful for modulating carboxylesterase-like enzyme gene expression. The
XX present sequence is carboxylesterase type-B serine peptide
XX
XX Sequence 41 AA;
XX
XX Query Match 6.0%; Score 35; DB 5; Length 41;
XX Best Local Similarity 100.0%; Pred. No. 6.4e-26;
XX Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 198 GNMARFQDVAAALSWQKNIIEFGDPSSVTYIGES 232
XX |||||
XX 1 GNMARFQDVAAALSWQKNIIEFGDPSSVTYIGES 35
XX
XX RESULT 28
XX ID ADF50145 standard; protein; 542 AA.
XX
XX ADF50145;
XX
XX 12-FEB-2004 (first entry)
XX
XX Cat cauxin protein SEQ ID NO:2.
XX
XX cat; cauxin; cat kidney disease marker; kidney disease.
XX
XX Felis catus.
XX
XX OS

```

```

XX JP2003250575-A.
XX
XX 09-SEP-2003.
XX
XX 04-MAR-2002; 2002JP-00057908.
XX
XX 04-MAR-2002; 2002JP-00057908.
XX
XX (TOHO-) TOHOKU TECHNOARCH KK.
XX
XX WPI, 2004-002277/01.
XX
XX N-PSDB; ADF50144.
XX
XX Novel cauxin protein or its salt, useful as a cat kidney disease marker,
XX and for diagnosing cat kidney disease.
XX
XX Claim 3; SEQ ID NO 2; 33pp; Japanese.
XX
XX The present sequence represents a cat cauxin protein (I) or its salt,
XX which is cat kidney disease marker. Also described: (1) a partial peptide
XX (II) of (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector
XX (IV) comprising (III); (4) a transformed host (V) comprising (III) or
XX (IV); (5) producing (I) or (II) by culturing (V); (6) an antibody (VI)
XX which couples specifically with (I) or (II); (7) diagnosing cat kidney
XX disease which involves measuring (I) quantitatively; (8) a reagent which
XX of amount of (I) indicates presence of the disease; and (9) a cauxin
XX disease diagnostic agent comprising (II) labelling agent, a reagent which
XX measures the biological activity of urinary (I) or (VI); and (9) a cauxin
XX detection kit which measures cauxin in a test sample. (I) is useful as a
XX cat kidney disease marker and (VI) is useful for diagnosing cat kidney
XX disease. (I) enables detection of cat kidney disease simply and
XX correctly. (I) provides an early marker for the disease, and replaces
XX complicated diagnostic methods such as X-ray imaging, ultrasonic imaging,
XX blood testing.
XX
XX Sequence 542 AA;
XX
XX Query Match 5.3%; Score 31; DB 8; Length 542;
XX Best Local Similarity 100.0%; Pred. No. 5.9e-21;
XX Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 465 RFVFGAFLKGDIVWFEGATEEKLRSKRM 495
XX |||||
XX 466 RFVFGAFLKGDIVWFEGATEEKLRSKRM 466
XX
XX RESULT 29
XX ID ADF50147 standard; protein; 542 AA.
XX
XX ADF50147;
XX
XX 12-FEB-2004 (first entry)
XX
XX Cat cauxin protein SEQ ID NO:4.
XX
XX cat; cauxin; cat kidney disease marker; kidney disease.
XX
XX Felis catus.
XX
XX OS
XX OS
XX JP2003250575-A.
XX
XX 09-SEP-2003.
XX
XX 04-MAR-2002; 2002JP-00057908.
XX
XX 04-MAR-2002; 2002JP-00057908.
XX
XX (TOHO-) TOHOKU TECHNOARCH KK.
XX
XX WPI, 2004-002277/01.
XX
XX N-PSDB; ADF50146.
XX

```

XX Novel cauxin protein or its salt, useful as a cat kidney disease marker,  
PT and for diagnosing cat kidney disease.  
XX  
XX  
PS Disclosure; SEQ ID NO 4; 33pp; Japanese.  
XX

CC The present sequence represents a cat cauxin protein (I) or its salt,  
CC which is cat kidney disease marker. Also described: (1) a partial peptide  
CC (II) of (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector  
CC (IV) comprising (III); (4) a transformed host (V) comprising (III) or  
CC (IV); (5) producing (I) or (II) by culturing (V); (6) an antibody (VI)  
CC which couples specifically with (I) or (II); (7) diagnosing cat kidney  
CC disease which involves measuring (I) quantitatively, and where reduction  
CC of amount of (I) indicates presence of the disease; (8) a cat kidney  
CC disease diagnostic agent comprising (I) labelling agent, a reagent which  
CC measures the biological activity of urinary (I) or (VI); and (9) a cauxin  
CC detection kit which measures cauxin in a test sample. (I) is useful as a  
CC cat kidney disease marker and (VI) is useful for diagnosing cat kidney  
CC disease. (I) enables detection of cat kidney disease simply and  
CC correctly. (I) provides an early marker for the disease, and replaces  
CC complicated diagnostic methods such as X-ray imaging, ultrasonic imaging,  
CC blood testing.  
XX

XX Sequence 542 AA;

Query Match 5.3%; Score 31; DB 8; Length 542;

Best Local Similarity 100.0%; Pred. No. 5.9e-21;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 465 RFVFGAFLKGDIVFEGATEEEXLSRKM 495  
|||||  
DB 456 RFVFGAFLKGDIVFEGATEEEXLSRKM 486

Search completed: June 16, 2005, 21:01:29  
Job time : 171 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 20:46:43 ; Search time 42 Seconds  
(without alignments)  
1330.999 Million cell updates/sec

Title: US-10-674-636-2

Perfect score: 581  
Sequence: 1 MPQGLTSSASQWCFFLIQP.....PLSSLTFLSLQPPFFFCAP 581

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 30

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR\_79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Length	ID	Description
---------------	----------------	--------	----	-------------

No matches found

Search completed: June 16, 2005, 21:02:15  
Job time : 42 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 20:54:53 ; Search time 180 Seconds  
(without alignments)  
1652.878 Million cell updates/sec

Title: US-10-674-636-2

Perfect score: 581  
Sequence: 1 MPOGILTSASQWCFLLIQP.....PLSLITFLSLQPPFFFCAP 581

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 30

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	551	94.8	575	2	Q6NTJ32
2	400	66.8	525	2	Q96DN9
3	329	56.6	469	2	Q8NBC8
4	101	17.4	361	2	Q95KH3
5	31	5.3	545	2	Q81034

#### ALIGNMENTS

RESULT 1  
Q6NTJ32 PRELIMINARY; PRT: 575 AA.  
AC Q6NTJ32: 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE FLJ1547 protein.  
GN Name=FLJ1547;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OC NCBI\_TaxID=9606;  
OX NCB1  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PCR rescued clones;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242601899;  
RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Altshuler S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ueda T.B., Toshitsugu S., Cantinot P., Prange C., Rana S.S., Loggellano N.A., Peters G.J., Adamson R.D., Mullaly S.J., Boak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallos D.E., Schermer A., Schein J.E., Jones S.J., Maiz M.A.,  
RA "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PCR rescued clones;  
RA Director MGC Project;  
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/11pase family.  
DR EMBL: BC069501; AAH69501.1;  
DR HSBP; P12337; IKA1.  
DR GO; GO:0003824; F:catalytic activity; IEA.  
DR InterPro; IPR002018; CarboxylesteraseB.  
DR InterPro; IPR000379; Ser. estere.  
DR Pfam; PF00135; Coesterase; 1.  
DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
DR KW Hydrolyase.  
SQ SEQUENCE 575 AA; 63926 MW; 6F5B735BDEFC9C09 CRC64;

Query Match 94.8%; Score 551; DB 2; Length 575;  
Best Local Similarity 100.0%; Pred. NO. 0;  
Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 31 GPSAEGPQNRNRLGWIQKQVTVLGSPPVNVVFLGPPAPPLGSLRTNPQAPSPMDNL  
DB 25 GPSAEGPQNRNRLGWIQKQVTVLGSPPVNVVFLGPPAPPLGSLRTNPQAPSPMDNL 84  
QY 91 REATSYPLCLQNSBWLDDQMLKVKYPKGVSEDCLYINIYAPAHADTGSKLPLVWF 150  
DB 85 REATSYPLCLQNSBWLDDQMLKVKYPKGVSEDCLYINIYAPAHADTGSKLPLVWF 144  
QY 151 PGGAFTGSSASTPFGSALAAYEDVLYVVOYRLGIFGFTTWDQAPGNMAFKQVAALS 210  
DB 145 PGGAFTGSSASTPFGSALAAYEDVLYVVOYRLGIFGFTTWDQAPGNMAFKQVAALS 204  
QY 211 WYQKNIFFFGDPSSTVFIFGESAGAI SVSLLISPMAGLPHKAIMESGVAIIIPYLEAHD 270  
DB 205 WYQKNIFFFGDPSSTVFIFGESAGAI SVSLLISPMAGLPHKAIMESGVAIIIPYLEAHD 264  
QY 271 YKSEEDLVVAHFCGNNA DSEALLRCRTYPSKELLTLISQKTSFTRVVDGAPFPNPL 330  
DB 265 YKSEEDLVVAHFCGNNA DSEALLRCRTYPSKELLTLISQKTSFTRVVDGAPFPNPL 324  
QY 331 DLSQKAKAIPSIIGVNNHCGFLIPKKEAPETLISGNSKSLALHLIONILHIPQYVHL 390  
DB 325 DLSQKAKAIPSIIGVNNHCGFLIPKKEAPETLISGNSKSLALHLIONILHIPQYVHL 384  
QY 391 VANEYFHHKSLTELRDSDLDLGDFVFPVLPALITARHRODAGAVYFEFRHRQCFED 450  
DB 385 VANEYFHHKSLTELRDSDLDLGDFVFPVLPALITARHRODAGAVYFEFRHRQCFED 444  
QY 451 TKPAFVKADHAEVRFVFGAFLKGDIVMEFGATEEEXLLSRKMKVATFARTGNPNCN 510  
DB 445 TKPAFVKADHAEVRFVFGAFLKGDIVMEFGATEEEXLLSRKMKVATFARTGNPNCN 504  
QY 511 DLSLMPANLLEQYIQLDLNMSLGRKLERVDPWTSTIPLILASDMLHPLSLSTFLS 570  
DB 505 DLSLMPANLLEQYIQLDLNMSLGRKLERVDPWTSTIPLILASDMLHPLSLSTFLS 564

OY 571 LLOPFFPCAP 561  
 DB 565 LLOPFFPCAP 575

## RESULT 2

096DN9 PRELIMINARY; PRT; 525 AA.  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 19, Last sequence update)  
 DE Hypothetical protein FLJ151547.  
 GN Name=FLJ151547;  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=14702039; DOI=10.1038/ng1285;  
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
 Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
 Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
 Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahata K.,  
 Murakami K., Yasuda T., Iwawaga T., Magatsuma M., Shintani A.,  
 Takahashi K., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,  
 Nishimura K., Ishihara T., Yamashita H., Murakawa K., Yamazaki M.,  
 Tanai H., Kimura M., Watanabe M., Hirose S., Chiba Y., Iehida S.,  
 Oono Y., Takiguchi S., Watanabe M., Hirose S., Chiba Y., Iehida S.,  
 Kanoori K., Takahashi F., Fujii A., Hara H., Tanase T., Kusano J.,  
 Togawa S., Kono T., Hara R., Takeuchi K., Arita M., Imose N.,  
 Musashino K., Yuki H., Oshima H., Sasaki N., Aotaka S.,  
 Moriya S., Mochiyama H., Ichihara T., Shiohara N., Sano S.,  
 Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H.,  
 Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kakikami B.,  
 Fujimori Y., Komiyama M., Tashiro H., Taniguchi A., Fujisawa T.,  
 Oono T., Yamada K., Fujii Y., Ozaki K., Hiro M., Ohmori Y.,  
 Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikemura Y., Okamoto S.,  
 Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
 Matsunura K., Nakajima T., Mizuno T., Morinaga M., Sasaki M.,  
 Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
 Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
 Okumura K., Nagase T., Nomura N., Kikuchi H., Maehara Y., Yamashita R.,  
 Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
 "Complete sequencing and characterization of 21,243 full-length human  
 cDNAs.";  
 Nat. Genet. 36:40-45(2004).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PCR rescued clones;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Bhat N.K.,  
 Hopkins R.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 Datchenko L., Marziani K., Farmer A.A., Rubin G.M., Hong L.,  
 Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abrahams R.D., Mullany S.J.,  
 Bosak S.A., McLean P.J., McKernan K.J., Malek J.A., Gunnarsson P.H.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettner M., Madan A.C., Rodriguez S., Sanchez A.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 Kravinsky M.I., Skalski U., Smalios D.E., Scherch A., Schein J.E.,  
 Jones S.J., Mair M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PCR rescued clones;  
 RA Straussberg R.;

Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/11pase family.  
 DR EMBL; AK056109; BAB71094.1; -  
 DR EMBL; BC069548; AAH69548.1; -  
 DR HSSP; P12337; 1K4Y.  
 DR GO; GO:0016787; F:hydrolyase activity; IEA.  
 DR InterPro; IPR002018; Carboxylesterase.  
 DR InterPro; IPR000379; Ser\_esterase.  
 DR Pfam; PF00135; Coesterase; 1.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KM Hydrolyase; Hypothetical protein.  
 SQ SEQUENCE 525 AA; 58200 MW; 7724878B8A22F215 CRC64;

Query Match 68.8%; Score 400; DB 2; Length 525;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 GRSAGGPOHNRRLGWIQKQVTVVGSFVNVVFLGVPFAPPLGSLRFTNPQASPMNDT 90  
 DB 25 GRSAGGPOHNRRLGWIQKQVTVVGSFVNVVFLGVPFAPPLGSLRFTNPQASPMNDT 84  
 OY 91 REATSYPNLCIONSEMLLDQMLKVPKFGVSEDCYLYNTVPAHADGSKLPVYVWF 150  
 DB 85 REATSYPNLCIONSEMLLDQMLKVPKFGVSEDCYLYNTVPAHADGSKLPVYVWF 144  
 OY 151 PGAGKTGSAISFGSALAAEDVLYVVOYRIGIFGFTTMDQAHAGNNAFKDOVAALS 210  
 DB 145 PGAGKTGSAISFGSALAAEDVLYVVOYRIGIFGFTTMDQAHAGNNAFKDOVAALS 204  
 OY 211 WVKNIIEFFGDPSSVITIFGFSAGAISSVSLISPMKGLFHRNIMESGVAITPYEAND 270  
 DB 205 WVKNIIEFFGDPSSVITIFGFSAGAISSVSLISPMKGLFHRNIMESGVAITPYEAND 264  
 OY 271 YEKEDDQVNAHFGGNASDSEALRCLRTKPSKELLTTSQKTSFTRVVDGAFPNNEPL 330  
 DB 265 YEKEDDQVNAHFGGNASDSEALRCLRTKPSKELLTTSQKTSFTRVVDGAFPNNEPL 324  
 OY 331 DLSQKAFKAIPISTIGVNHCEGFLPMKEAPETILSGNSKSLALHILQNIHLIPPOYLH 390  
 DB 325 DLSQKAFKAIPISTIGVNHCEGFLPMKEAPETILSGNSKSLALHILQNIHLIPPOYLH 384  
 OY 391 VANEYFHDKSLTEIRDSLLDLGDFVFFVVPALITARYR 430  
 DB 385 VANEYFHDKSLTEIRDSLLDLGDFVFFVVPALITARYR 424

## RESULT 3

08NBC8 PRELIMINARY; PRT; 469 AA.  
 AC 08NBC8;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein FLJ3678.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX PubMed=14702039; DOI=10.1038/ng1285;  
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
 Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
 Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

Query Match	56.6%	Score 329	DB 2	Length 469
Best Local Similarity	99.8%	Pred. No. 0		
Matches 429	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY	113	MLKHYHPKGVSEDLINIIYAPAHADTGSKLPIVLWPFPGAFTGASIFDGSAIAYE	172	
Db	1	MLKHYHPKGVSEDLINIIYAPAHADTGSKLPIVLWPFPGAFTGASIFDGSAIAYE	60	
QY	173	DVLVWVVOYRIGIPGFPTTDOHA.PGNMA.FPDQVAAISMVQNIIEFGADGSSVITFGES	232	
Db	61	DVLVWVVOYRIGIPGFPTTDOHA.PGNMA.FPDQVAAISMVQNIIEFGADGSSVITFGES	120	
QY	233	AGAISVSLIISPMAKGLFHKAIMEGVAIIPYLEAHDYKESIEDIQVAHFCGNAASDSE	292	
Db	121	AGAISVSLIISPMAKGLFHKAIMEGVAIIPYLEAHDYKESIEDIQVAHFCGNAASDSE	180	
QY	293	ALLRCLATPBEKELLTSQTKTSFTRVVDGAFPMPEBIDLSQKAFKAPSTIGNNHEC	352	
Db	181	ALLRCLATPBEKELLTSQTKTSFTRVVDGAFPMPEBIDLSQKAFKAPSTIGNNHEC	240	
QY	353	GFLLPMEKAEPIILSGSNSLALHLIQLNIILH.IPPQYILLVANEEYFHDKSLTEIRDSLDL	412	
Db	241	GFLLPMEKAEPIILSGSNSLALHLIQLNIILH.IPPQYILLVANEEYFHDKSLTEIRDSLDL	300	
QY	413	LGDVFPVVPALITRHYRDAGAPVTFYEFRRPQCFEDTTRKAPFVADHADERPFGGAF	472	
Db	301	LGDVFPVVPALITRHYRDAGAPVTFYEFRRPQCFEDTTRKAPFVADHADERPFGGAF	360	
QY	473	LKGDIVMEFEGATEEBKLSLRQMKMKWATFAATGNGNDLSLMPAYNLTBOYLQGLDNMS	532	
Db	361	LKGDIVMEFEGATEEBKLSLRQMKMKWATFAATGNGNDLSLMPAYNLTBOYLQGLDNMS	420	
QY	533	LGQRILKEPRV	542	

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Db      421 LGGRLKEPRV 430  
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RESULT 4

ID		PRT;	361 AA.
AC	O95KH3 PRELIMINARY;		
DT	01-DEC-2001 (TREMBlrel_19, Created)		
DT	01-DEC-2001 (TREMBlrel_19, Last sequence update)		
DT	01-OCT-2003 (TREMBlrel_25, Last annotation update)		
DE	Hypothetical protein.		
OC	Macaque fascicularis (Crab eating macaque) ( <i>Cynomolgus monkey</i> ).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;		
OX	Cercopithecinae; Macaca.		
NCBI_TaxID=9541;			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-Temporal lobe right;		
RA	Oaeda N., Hida M., Kiyoda J., Tanuma R., Iseki K., Hirai M., Terao K.,		
RA	Suzuki Y., Sugano S., Hashimoto K.;		
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.		
-1-	SMILIARITY: Belongs to the type-B carboxylesterase/lipase family.		
DR	EMBL: AB060873; BAB46884.1; -.		
DR	HSSP: P12337; 1K4Y		
DR	InferPro: IPRO02018; CarbesteraseB.		
DR	Pfam: PF00135; Coesterase; 1.		
KW	Hypothetical protein.		
SO	SEQUENCE 361 AA; 41032 MW; AC62AB6E78C5F1A1 CRC64;		

Query Match            17.4%; Score 101; DB 2; Length 361;  
Best Local Similarity 100.0%; Pred.No. 1.5e-93;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy       409 LLDLIGVFVVVALITARYRHDAAGAVVYYEFRRHQCEEDTPAFVKADHAEVAFFV 468  
|||  
Ddb      183 LLHLGDFEVFPPLIARIHRHDGAIFYTYFERHNRQCCEDTIKPAFYKDHAEVAFVF 242  
|||  
  
        469 GAFLKGDIWMFGATTEEEKLLSRKKMKYMATPARTGNPG 509  
|||  
Ddb      243 GAFLKGDIWMFGATTEEEKLLSRKKMKYMATPARTGNPNNG 283  
|||

RESULT 5

ID		PRT;	545 AA.
AC	O81034 PRELIMINARY;		
DT	01-MAR-2003 (TREMBlrel_23, Created)		
DT	01-MAR-2003 (TREMBlrel_23, Last sequence update)		
DT	01-OCT-2003 (TREMBlrel_25, Last annotation update)		
DE	Carboxylesterase-like urinary excreted protein.		
Gn	Name-Cauxin;		
OS	Felis silvestris catus (Cat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Carnivora; Fissipedidae; Felidae; Felis.		
NCBI_TaxID=9685;			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-Kidney;		
RX	MEDLINE:22458314; PubMed=12401131; DOI=10.1042/BJ20021446;		
RA	Miyazaki M., Kamih K., Soeta S., Tsura H., Yamashita T.;		
RT	"Molecular cloning and characterization of a novel carboxylesterase- like protein that is physiologically present at high concentrations in the urine of domestic cats (Felis catus).";		
Biochem_J	370:101-110(2003).		
-1-	SMILIRITY: Belongs to the type-B carboxylesterase/lipase family.		
DR	EMBL: AB045377; BACC2577.1; --.		
DR	HSSP: P12337; 1K4Y.		
DR	GO: GO:0016787; F:hydrolase activity; IEA.		
DR	InferPro: IPRO02018; CarbesteraseB.		
DR	InferPro: IPRO00379; Ser estra.		
pflam:	PF00135; Coesterase; 1.		

DR PROSITE, PS00122; CARBOXYLESTERASE\_B\_1; 1.  
DR PROSITE, PS00941; CARBOXYLESTERASE\_B\_2; 1.  
KW Hydrolase.  
SQ SEQUENCE 545 AA; 60505 MW; 9F73FA693D271FA9 CRC64;

Query Match 5.3%; Score 31; DB 2; Length 545;  
Best Local Similarity 100.0%; Pred. No. 4.4e-22;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 RFVFGAFLKGDIVMEGATEEEKLSRKM 495  
|||  
Db 459 RFVFGAFLKGDIVMEGATEEEKLSRKM 489

Search completed: June 16, 2005, 21:05:22  
Job time : 181 secs



GenCore version 5.1.6  
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OM protein - protein search, using BW model

Run on: June 16, 2005, 20:55:54 ; Search time 43 Seconds  
(without alignments)  
1008.630 Million cell updates/sec

Title: US-10-674-636-2

Perfect score: 581  
Sequence: 1 MPQGLTSSASQWCFLLIQP.....PLSLTFLSLQPFFFFCAP 581

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size: 30

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database:

Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	581	100.0	581	4	US-10-023-515-2 Sequence 2, Appl1

#### ALIGNMENTS

RESULT 1  
US-10-023-515-2  
Sequence 2, Application US/10023515  
Patent No. 6664091  
GENERAL INFORMATION:  
APPLICANT: Curtis, Rory A. J.  
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYL ESTERASE  
FILE REFERENCE: 10448-122001  
CURRENT APPLICATION NUMBER: US/10/023,515  
CURRENT FILING DATE: 2001-12-18  
PRIOR APPLICATION NUMBER: 60/256,369  
PRIOR FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: 60/279,508  
PRIOR FILING DATE: 2001-03-28  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 581  
TYPE: PRT

ORGANISM: Homo sapiens  
US-10-023-515-2

Query Match 100.0%; Score 581; DB 4; Length 581;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MPQGLTSSASQWCFLLIQPLIGHROWGKTGPSAEGFORTRLGMOGQVTVLGSPPV 60
DB	1	MPQGLTSSASQWCFLLIQPLIGHROWGKTGPSAEGFORTRLGMOGQVTVLGSPPV 60
QY	61	NVFLGVPPAAPPLGSLRFTNPQPASPWDNIREATSYNLCIQNSEWLLDQMLKHYPK 120
DB	61	NVFLGVPPAAPPLGSLRFTNPQPASPWDNIREATSYNLCIQNSEWLLDQMLKHYPK 120
QY	121	FGVSEDCLYNINYPARADGSKLPVWVPFGAFKTSASIFPGSALAAVEDLVVVVQ 180
DB	121	FGVSEDCLYNINYPARADGSKLPVWVPFGAFKTSASIFPGSALAAVEDLVVVVQ 180
QY	181	YRLGIFGFFTTWDQAHQNNAFKQVVAALSVQKNIEFFGSDPSVYIFGSSAGASVSS 240
DB	181	YRLGIFGFFTTWDQAHQNNAFKQVVAALSVQKNIEFFGSDPSVYIFGSSAGASVSS 240
QY	241	LILSPMAKGLFHKAIMESGVAIIPYLEADHYEKSEDLQVVAHFCGNNASDSEALLRCLRT 300
DB	241	LILSPMAKGLFHKAIMESGVAIIPYLEADHYEKSEDLQVVAHFCGNNASDSEALLRCLRT 300
QY	301	KPSKELLTTSOKTSFTRVVDGAFEPNEPLDLSOKAFKAIPTIIGVNNHCGFLPWKE 360
DB	301	KPSKELLTTSOKTSFTRVVDGAFEPNEPLDLSOKAFKAIPTIIGVNNHCGFLPWKE 360
QY	361	APETLSGNSKSLAHLIQLNIHIPPQYLHLVANEYFHDKISLTERISLIDLGDVFEVV 420
DB	361	APETLSGNSKSLAHLIQLNIHIPPQYLHLVANEYFHDKISLTERISLIDLGDVFEVV 420
QY	421	PALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVADHAEVRFVFGAFLKGDIVMF 480
DB	421	PALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVADHAEVRFVFGAFLKGDIVMF 480
QY	481	EGATEEEKLSRKKMKWTATFATGPNNGNDLSIWPAYNLTEOYLQDLNNLSLQRLKEP 540
DB	481	EGATEEEKLSRKKMKWTATFATGPNNGNDLSIWPAYNLTEOYLQDLNNLSLQRLKEP 540
QY	541	RVDFTSTIPLILSASDMLHSLSLTFLSLQPFFFFCAP 581
DB	541	RVDFTSTIPLILSASDMLHSLSLTFLSLQPFFFFCAP 581

Search completed: June 16, 2005, 21:06:11  
Job time : 43 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 21:02:21 ; Search time 159 Seconds  
(without alignments)  
1403.095 Million cell updates/sec

Title: US-10-674-636-2

Perfect score: 581  
Sequence: 1 MPOGUTSASQWCFLLIQP.....PLSLTFLSLIQPFPPFCAP 581

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1714042 seqs, 383979560 residues

Word size : 30

Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

Published Applications\_AA:\*

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*

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5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/2/pubpaa/US09D\_NEW\_PUB.pep:\*

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17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep:\*

18: /cgn2\_6/ptodata/2/pubpaa/US10F\_NEW\_PUB.pep:\*

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21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	581	100.0	581	US-10-023-515-2	Sequence 2, Appl1
2	581	100.0	581	US-10-674-636-2	Sequence 2, Appl1
3	581	100.0	581	US-10-757-262-46	Sequence 46, Appl1
4	551	96.8	575	US-10-451-168-91	Sequence 91, Appl1
5	400	66.8	525	US-10-094-749-2375	Sequence 2375, Appl1
6	381	65.6	525	US-10-433-256-10	Sequence 10, Appl1
7	340	58.5	356	US-10-451-168-93	Sequence 93, Appl1
8	329	58.6	469	US-10-104-047-2219	Sequence 2219, Appl1
9	328	58.5	581	US-10-114-270-196	Sequence 196, Appl1
10	328	58.5	581	US-10-451-168-92	Sequence 92, Appl1
11	328	56.5	618	US-10-381-898-2	Sequence 2, Appl1

12	49	8.4	49	9	US-09-864-761-36376	Sequence 36376, A
13	31	5.3	542	16	US-10-233-933A-2	Sequence 2, Appl1
14	31	5.3	542	16	US-10-233-933A-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1  
US-10-023-515-2  
Sequence 2, Application US/10023515  
Publication No. US20020182636A1  
GENERAL INFORMATION:  
APPLICANT: Curtis, Rory A. J.  
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYESTERASE  
TITLE OF INVENTION: FAMILY MEMBER AND USRS THEREOF  
FILE REFERENCE: 10448-122001  
CURRENT APPLICATION NUMBER: US/10/023, 515  
CURRENT FILING DATE: 2001-12-18  
PRIOR APPLICATION NUMBER: 60/256,369  
PRIOR FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: 60/279, 508  
PRIOR FILING DATE: 2001-03-28  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FASTSEQ, for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 581  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-023-515-2

Query Match 100.0%; Score 581; DB 13; Length 581;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	MPOGUTSASQWCFLLIQPILGHRQWKTGPSAEGPQRNRLGWIQKQVTVLGSPPV	60
QY	61	NVFLGVPAAAPPLGSLRTNPQSPMDNLEAITSYPLCTQNSWMLLDHMLKVHPK	120
DB	61	NVFLGVPAAAPPLGSLRTNPQSPMDNLEAITSYPLCTQNSWMLLDHMLKVHPK	120
QY	121	FGVSEDCLYLTIYAPAHADTGSKLPLYWPPGAFKTSASIFDGSALAAVEDVYLVVQ	180
DB	121	FGVSEDCLYLTIYAPAHADTGSKLPLYWPPGAFKTSASIFDGSALAAVEDVYLVVQ	180
QY	181	YRLGIFGFTTMDQAPGNMAFKQVVALSWQKNIIEFGDPSVTIFGSAGASVSS	240
DB	181	YRLGIFGFTTMDQAPGNMAFKQVVALSWQKNIIEFGDPSVTIFGSAGASVSS	240
QY	241	LILSPMAKGLFHAKIMESGVAIIPLYLAHDYKESDLOVVAHFCGNNASDBSALRCIRT	300
DB	241	LILSPMAKGLFHAKIMESGVAIIPLYLAHDYKESDLOVVAHFCGNNASDBSALRCIRT	300
QY	301	KPSKELLTSLQKTSFTRVVDGAFPPNRLDLSQAKAIPSTIGVNNHEGFLPKMB	360
DB	301	KPSKELLTSLQKTSFTRVVDGAFPPNRLDLSQAKAIPSTIGVNNHEGFLPKMB	360
QY	361	APELLGSNKLALHLIIONILHIPPOYLALVANEFFHDKSLTEIRDSLLDLGDPFVV	420
DB	361	APELLGSNKLALHLIIONILHIPPOYLALVANEFFHDKSLTEIRDSLLDLGDPFVV	420
QY	421	PALITARYHRDAGAPVYFEFRHRPQCEDTKPAVKADHAEVRFVFGAFPKKDIYMF	480
DB	421	PALITARYHRDAGAPVYFEFRHRPQCEDTKPAVKADHAEVRFVFGAFPKKDIYMF	480
QY	481	EGATEEELSLSRKMKWATFARTGNPNNGDLSLMPAYNLTEOYLQDLNNSIGORLEK	540
DB	481	EGATEEELSLSRKMKWATFARTGNPNNGDLSLMPAYNLTEOYLQDLNNSIGORLEK	540
QY	541	RVDFTSTIPLILSASDMLHSLSLTFLSLIQPFPPFCAP 581	

Db 541 RVDFTSTTPLLISASDMLHSPUSLTLFLSLQPFPPFCAP 581

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RESULT 2
US-10-674-636-2
; Sequence 2: Application US/10674636
; Publication No. US20040086922A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
; FILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/674,636
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/10/023,515
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,369
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-674-636-2
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Query Match 100.0%; Score 581; DB 15; Length 581;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MPOGLTSSASQWCFLLIOLPLGHRQWKTGPSAEGFORNTRLGMIOGQVTVLGSFPV 60
QY 61 NVFLGVFPFAAPPLGSLRFTNPOPASPMWDLREATSYPNCLQNSEWMLLDQHLKTHYRK 120
Db 61 NVFLGVFPFAAPPLGSLRFTNPOPASPMWDLREATSYPNCLQNSEWMLLDQHLKTHYRK 120
QY 121 FGVSIEDCLYNTIYAPAHADTGSKLPLYVWFPFGAFKTSASIFDGSALAAYEDVLVVVQ 180
Db 121 FGVSIEDCLYNTIYAPAHADTGSKLPLYVWFPFGAFKTSASIFDGSALAAYEDVLVVVQ 180
QY 181 YRLGIRFETFTTQOHAFGNMAFQDOVAALSWQKNIIEFFGSDPSVTIFGESAGAISVS 240
Db 181 YRLGIRFETFTTQOHAFGNMAFQDOVAALSWQKNIIEFFGSDPSVTIFGESAGAISVS 240
QY 241 LILSPMAKGLFHKAIMESGVAIIPYLEAHDYKSEDLQVVAHFCGNASDSEALLRCLRT 300
Db 241 LILSPMAKGLFHKAIMESGVAIIPYLEAHDYKSEDLQVVAHFCGNASDSEALLRCLRT 300
QY 301 KPEKELLTTSQKTSFTRVVDGAFPPNEPLDLLSQAFKAIPSIIGVNNHEGCFLLPMKE 360
Db 301 KPEKELLTTSQKTSFTRVVDGAFPPNEPLDLLSQAFKAIPSIIGVNNHEGCFLLPMKE 360
QY 361 APETILSGNSKSLALHILQNIHITPROYLIVANEYHHDGSLTETIDSLDLGLGVFPV 420
Db 361 APETILSGNSKSLALHILQNIHITPROYLIVANEYHHDGSLTETIDSLDLGLGVFPV 420
QY 421 PALITARYHRDAGAPYFYEFRHRPQCFEDTRKPAFKADHADVFPVFGAFLKGDYWF 480
Db 421 PALITARYHRDAGAPYFYEFRHRPQCFEDTRKPAFKADHADVFPVFGAFLKGDYWF 480
QY 481 EGATBEKSLSRKMKMYATPARTGNPNNDLSLWPAYNLTEQYLQDLNMSLQRLKEP 540
Db 481 EGATBEKSLSRKMKMYATPARTGNPNNDLSLWPAYNLTEQYLQDLNMSLQRLKEP 540
QY 541 RVDFTSTTPLLISASDMLHSPUSLTLFLSLQPFPPFCAP 581
Db 541 RVDFTSTTPLLISASDMLHSPUSLTLFLSLQPFPPFCAP 581
```

```
RESULT 3
US-10-757-262-46
; Sequence 46: Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Eliaouf, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 16560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 22077, 22245, 22877, 52308, 69112, 14990,
; TITLE OF INVENTION: 19547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE REFERENCE: MP103-007P1RNMNM
; CURRENT APPLICATION NUMBER: US/10/757,262
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-757-262-46

Query Match 100.0%; Score 581; DB 16; Length 581;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPOGLTSSASQWCFLLIOLPLGHRQWKTGPSAEGFORNTRLGMIOGQVTVLGSFPV 60
Db 1 MPOGLTSSASQWCFLLIOLPLGHRQWKTGPSAEGFORNTRLGMIOGQVTVLGSFPV 60
QY 61 NVFLGVFPFAAPPLGSLRFTNPOPASPMWDLREATSYPNCLQNSEWMLLDQHLKTHYRK 120
Db 61 NVFLGVFPFAAPPLGSLRFTNPOPASPMWDLREATSYPNCLQNSEWMLLDQHLKTHYRK 120
QY 121 FGVSIEDCLYNTIYAPAHADTGSKLPLYVWFPFGAFKTSASIFDGSALAAYEDVLVVVQ 180
Db 121 FGVSIEDCLYNTIYAPAHADTGSKLPLYVWFPFGAFKTSASIFDGSALAAYEDVLVVVQ 180
QY 181 YRLGIRFETFTTQOHAFGNMAFQDOVAALSWQKNIIEFFGSDPSVTIFGESAGAISVS 240
Db 181 YRLGIRFETFTTQOHAFGNMAFQDOVAALSWQKNIIEFFGSDPSVTIFGESAGAISVS 240
QY 241 LILSPMAKGLFHKAIMESGVAIIPYLEAHDYKSEDLQVVAHFCGNASDSEALLRCLRT 300
Db 241 LILSPMAKGLFHKAIMESGVAIIPYLEAHDYKSEDLQVVAHFCGNASDSEALLRCLRT 300
```

Db 241 LILSPMAKGLFHKAIMESGVAIIIPYLEANDYKESDLOVVAHFCGNNA SDEBALRCURT 300  
Qy 301 KPSEKELLTSQKTSFTRVVDGAFPPNEPLDLSQKAFKAIPSIIGVNNHCGFLLPKKE 360  
Db 301 KPSEKELLTSQKTSFTRVVDGAFPPNEPLDLSQKAFKAIPSIIGVNNHCGFLLPKKE 360  
Qy 361 APEILSGNSKSLAHLIIONIIHIPPOYLHVA NEYFHDKSLTEIRDSLDLGDVFFV 420  
Db 361 APEILSGNSKSLAHLIIONIIHIPPOYLHVA NEYFHDKSLTEIRDSLDLGDVFFV 420  
Qy 421 PALTAARHARAGAPVYFEFRHRPQCEPDTRKPAVKADHDEVRFVGCAPFLKGDIMF 480  
Db 421 PALTAARHARAGAPVYFEFRHRPQCEPDTRKPAVKADHDEVRFVGCAPFLKGDIMF 480  
Qy 481 EGATEEEKLSRKKMKYATFARTGNPAGNDLSLWPAVNLTEOYLQDLNMSLGRLKEP 540  
Db 481 EGATEEEKLSRKKMKYATFARTGNPAGNDLSLWPAVNLTEOYLQDLNMSLGRLKEP 540  
Qy 541 RVDFWTSTIPLILSASDMLHSPLSLFTLSLLOPPFFCAP 581  
Db 541 RVDFWTSTIPLILSASDMLHSPLSLFTLSLLOPPFFCAP 581

## RESULT 4

US-10-451-168-91  
Sequence 91, Application US/10451168  
Publication No. US20040091969A1  
GENERAL INFORMATION:  
APPLICANT: SMITHKLINE BEECHAM CORPORATION  
APPLICANT: GLAXO GROUP LIMITED  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GP50039  
CURRENT APPLICATION NUMBER: US/10/451,168  
CURRENT FILING DATE: 2003-11-12  
PRIOR APPLICATION NUMBER: PCT/US01/49232  
PRIOR FILING DATE: 2000-12-17  
PRIOR APPLICATION NUMBER: 60/256,710  
PRIOR FILING DATE: 2000-12-19  
PRIOR APPLICATION NUMBER: 60/257,048  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 60/260,482  
PRIOR FILING DATE: 2001-01-09  
PRIOR APPLICATION NUMBER: 60/264,922  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: 60/266,797  
PRIOR FILING DATE: 2001-02-06  
PRIOR APPLICATION NUMBER: 60/276,988  
PRIOR FILING DATE: 2001-03-19  
PRIOR APPLICATION NUMBER: 60/281,535  
PRIOR FILING DATE: 2001-04-04  
PRIOR APPLICATION NUMBER: 60/289,622  
PRIOR FILING DATE: 2002-06-28  
NUMBER OF SEQ ID NOS: 110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 91  
LENGTH: 575  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-451-168-91

Query Match 94.8%; Score 551; DB 15; Length 575;  
Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;  
Matches 551; Conservative 0; Mismatches 0;

Qy 31 GPSAGPQRNTRLGWIQSGQVTVLGSVPVNVFLGVPAAPLGLRFTNPQAPMNDL 90  
Db 25 GPSAGPQRNTRLGWIQSGQVTVLGSVPVNVFLGVPAAPLGLRFTNPQAPMNDL 84  
Qy 91 REATISYVULCLONSWLLLDQMLKVHYPKRGVSEDCLYNTIYAAHADTGSKLPLVLMF 150  
Db 85 REATISYVULCLONSWLLLDQMLKVHYPKRGVSEDCLYNTIYAAHADTGSKLPLVLMF 144

Qy 151 PGCAFPTGSASIFPGSALAAVEDLVVVVVOYRLGIFGFPTTMDQHAPGNMAFKQVVALS 210  
Db 145 PGCAFPTGSASIFPGSALAAVEDLVVVVVOYRLGIFGFPTTMDQHAPGNMAFKQVVALS 204  
Qy 211 WVOGNIEFGDPSVITIFGSAGAISSVSLILSPMAKGLFHKAIMESGVAIIIPYLEAND 270  
Db 205 WVOGNIEFGDPSVITIFGSAGAISSVSLILSPMAKGLFHKAIMESGVAIIIPYLEAND 264  
Qy 271 YKESDLOVVAHFCGNNA SDEBALRCURTSPKELLTSQKTSFTRVVDGAFPPNEPL 330  
Db 265 YKESDLOVVAHFCGNNA SDEBALRCURTSPKELLTSQKTSFTRVVDGAFPPNEPL 324  
Qy 331 DLSQKAFKAIPSIIGVNNHCGFLLPKKEAPEILSGNSKSLAHLIIONIIHIPPOYLH 390  
Db 325 DLSQKAFKAIPSIIGVNNHCGFLLPKKEAPEILSGNSKSLAHLIIONIIHIPPOYLH 384  
Qy 391 VANEYFHDKSLTEIRDSLDLGDVFFVVPALITARHARAGAPVYFEFRHRPQCEPD 450  
Db 385 VANEYFHDKSLTEIRDSLDLGDVFFVVPALITARHARAGAPVYFEFRHRPQCEPD 444  
Qy 451 TKPAFVADHDEVRFVGCAPFLKGDIMFEGATEEEKLSRKKMKYATFARTGNPAGN 510  
Db 445 TKPAFVADHDEVRFVGCAPFLKGDIMFEGATEEEKLSRKKMKYATFARTGNPAGN 504  
Qy 511 DLSMPAYNLTEOYLQDLNMSLGRLKEPVDFTWTSTIPLILSASDMLHSPLSLFTLS 570  
Db 505 DLSMPAYNLTEOYLQDLNMSLGRLKEPVDFTWTSTIPLILSASDMLHSPLSLFTLS 564  
Qy 571 LLOPPFFCAP 581  
Db 565 LLOPPFFCAP 575

## RESULT 5

US-10-094-749-2375  
Sequence 2375, Application US/10094749  
Publication No. US20030219741A1  
GENERAL INFORMATION:  
APPLICANT: ISOGAI, TAKAO  
APPLICANT: SUGIYAMA, TOMOYASU  
APPLICANT: OTSUKI, TETSUJI  
APPLICANT: WAKAMATSU, AI  
APPLICANT: SATO, HIROYUKI  
APPLICANT: ISHII, SHIZUKO  
APPLICANT: YAMAMOTO, JUN-ICHI  
APPLICANT: ISONO, YUUKO  
APPLICANT: HIO, YURI  
APPLICANT: OTSUKA, KAORU  
APPLICANT: NAGAI, KEIICHI  
APPLICANT: IRIE, RYOTARO  
APPLICANT: TAMECHIKA, ICHIRO  
APPLICANT: SEKI, NAOHICO  
APPLICANT: YOSHIKAWA, TSUTOMU  
APPLICANT: OTSUKA, MOTOKUJI  
APPLICANT: NAGAHARI, KENJI  
APPLICANT: MASUHO, YASUHIKO  
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA  
FILE REFERENCE: 084335/0160  
CURRENT APPLICATION NUMBER: US/10/094,749  
CURRENT FILING DATE: 2002-03-12  
PRIOR APPLICATION NUMBER: 60/350,435  
PRIOR FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: JP 2001-328381  
PRIOR FILING DATE: 2001-09-14  
NUMBER OF SEQ ID NOS: 3381  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2375  
LENGTH: 525  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-094-749-2375

Query Match 68.8%; Score 400; DB 15; Length 525;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 31 GSAAGPQNTRLGWIQKQVTVLGSFVFNVFLGVFAAPPLGSLRFTNPPASPMNDL 90
DB 25 GSAAGPQNTRLGWIQKQVTVLGSFVFNVFLGVFAAPPLGSLRFTNPPASPMNDL 84
QY 91 REATSYPNICLQNSEWMLLDQHLKVHYPKFVSEDCLYLNIYAPAHADTGSKLPLYWF 150
DB 85 REATSYPNICLQNSEWMLLDQHLKVHYPKFVSEDCLYLNIYAPAHADTGSKLPLYWF 144
QY 151 PGAFKTSASIFDGSALAAVEDLVVVVQYRLGIFGFPTTMDQAPGNMAFKQVAAALS 210
DB 145 PGAFKTSASIFDGSALAAVEDLVVVVQYRLGIFGFPTTMDQAPGNMAFKQVAAALS 204
QY 211 WQKNIIEFGDPPSSVTIFGESAGAISSVSLISPMAGLPHKAIMESGVAIIPYLEAHD 270
DB 205 WQKNIIEFGDPPSSVTIFGESAGAISSVSLISPMAGLPHKAIMESGVAIIPYLEAHD 264
QY 271 YEKSEDLQVVAHFCGNMNSDEBALRCLRTKPSKELLTISQKTSFTRVVDGAFPPNEPL 330
DB 265 YEKSEDLQVVAHFCGNMNSDEBALRCLRTKPSKELLTISQKTSFTRVVDGAFPPNEPL 324
QY 331 DLSQKAFKAIPIIIGVNNHECGFLLPMKEAPEILSGNSKSLAHLQNTLIHIPQYVHL 390
DB 325 DLSQKAFKAIPIIIGVNNHECGFLLPMKEAPEILSGNSKSLAHLQNTLIHIPQYVHL 384
QY 391 VANEFPHDKSLTEIRDSLLDLGDFVFPVVALITARYHR 430
DB 385 VANEFPHDKSLTEIRDSLLDLGDFVFPVVALITARYHR 424
```

## RESULT 6

US-10-433-256-10  
Sequence 10, Application US/10433256  
Publication No. US20040081980A1  
GENERAL INFORMATION:  
APPLICANT: SANJANWALA, Madhusudan M.; YAO, Monique G.  
APPLICANT: AU-YOUNG, Janice K.; BAUGHN, Mariah R.  
APPLICANT: ARVIZU, Chandra S.; RING, Huijun Z.  
APPLICANT: LEE, Ernestine A.; DING, Li  
APPLICANT: HAPALIA, April J.A.; TANG, Y. Tom  
APPLICANT: YUE, Henry; TRIBOULEY, Catherine M.  
APPLICANT: LU, Dying; Alina M.; LAL, Preeci G.  
APPLICANT: WARREN, Bridget A.; YANG, Junming  
APPLICANT: CHAMLA, Narinder K.; NGUYEN, Damiel B.  
APPLICANT: GANDHI, Ameena R.; LU, Yan  
APPLICANT: ISON, Craig H.  
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES  
FILE REFERENCE: PI-0313 USN  
CURRENT APPLICATION NUMBER: US/10/433,256  
PRIOR FILING DATE: 2003-05-30  
PRIOR APPLICATION NUMBER: PCT/US01/47429  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: US 60/254,308  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: US 60/256,189  
PRIOR FILING DATE: 2000-12-15  
PRIOR APPLICATION NUMBER: US 60/257,713  
PRIOR FILING DATE: 2000-12-21  
PRIOR APPLICATION NUMBER: US 60/262,706  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: US 60/266,020  
PRIOR FILING DATE: 2001-02-02  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PERL Program  
SEQ ID NO 10  
LENGTH: 642  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No: 6538080CD1

## US-10-433-256-10

Query Match 65.6%; Score 381; DB 15; Length 642;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 31 GSAAGPQNTRLGWIQKQVTVLGSFVFNVFLGVFAAPPLGSLRFTNPPASPMNDL 90
DB 92 GSAAGPQNTRLGWIQKQVTVLGSFVFNVFLGVFAAPPLGSLRFTNPPASPMNDL 151
QY 91 REATSYPNICLQNSEWMLLDQHLKVHYPKFVSEDCLYLNIYAPAHADTGSKLPLYWF 150
DB 152 REATSYPNICLQNSEWMLLDQHLKVHYPKFVSEDCLYLNIYAPAHADTGSKLPLYWF 211
QY 151 PGAFKTSASIFDGSALAAVEDLVVVVQYRLGIFGFPTTMDQAPGNMAFKQVAAALS 271
DB 212 PGAFKTSASIFDGSALAAVEDLVVVVQYRLGIFGFPTTMDQAPGNMAFKQVAAALS 271
QY 211 WQKNIIEFGDPPSSVTIFGESAGAISSVSLISPMAGLPHKAIMESGVAIIPYLEAHD 270
DB 272 WQKNIIEFGDPPSSVTIFGESAGAISSVSLISPMAGLPHKAIMESGVAIIPYLEAHD 331
QY 271 YEKSEDLQVVAHFCGNMNSDEBALRCLRTKPSKELLTISQKTSFTRVVDGAFPPNEPL 330
DB 332 YEKSEDLQVVAHFCGNMNSDEBALRCLRTKPSKELLTISQKTSFTRVVDGAFPPNEPL 391
QY 331 DLSQKAFKAIPIIIGVNNHECGFLLPMKEAPEILSGNSKSLAHLQNTLIHIPQYVHL 390
DB 392 DLSQKAFKAIPIIIGVNNHECGFLLPMKEAPEILSGNSKSLAHLQNTLIHIPQYVHL 451
QY 391 VANEFPHDKSLTEIRDSLLDLGDFVFPVVALITARYHRDAGAVYFEFRHRPQCED 450
DB 452 VANEFPHDKSLTEIRDSLLDLGDFVFPVVALITARYHRDAGAVYFEFRHRPQCED 511
QY 451 TKPAFVKADHDEVRFVVGAFILKGDIVMFGATEEBELSRKMKYATFARTGNBGN 510
DB 512 TKPAFVKADHDEVRFVVGAFILKGDIVMFGATEEBELSRKMKYATFARTGNBGN 571
QY 511 DL 512
DB 572 DL 573
```

## RESULT 7

US-10-451-168-93  
Sequence 93, Application US/10451168  
Publication No. US20040091969A1  
GENERAL INFORMATION:  
APPLICANT: SMITHKLINE BEECHAM CORPORATION  
APPLICANT: SMITHKLINE BEECHAM P.L.C.  
APPLICANT: GLAXO GROUP LIMITED  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GP50039  
CURRENT APPLICATION NUMBER: US/10/451,168  
PRIOR FILING DATE: 2003-11-12  
PRIOR APPLICATION NUMBER: PCT/US01/49232  
PRIOR FILING DATE: 2000-12-17  
PRIOR APPLICATION NUMBER: 60/256,710  
PRIOR FILING DATE: 2000-12-19  
PRIOR APPLICATION NUMBER: 60/257,048  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 60/260,482  
PRIOR FILING DATE: 2001-01-09  
PRIOR APPLICATION NUMBER: 60/264,922  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: 60/266,797  
PRIOR FILING DATE: 2001-02-06  
PRIOR APPLICATION NUMBER: 60/276,988  
PRIOR FILING DATE: 2001-03-19  
PRIOR APPLICATION NUMBER: 60/281,535  
PRIOR FILING DATE: 2001-04-04  
PRIOR APPLICATION NUMBER: 60/289,622  
PRIOR FILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 93  
LENGTH: 356  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-451-168-93

Query Match 58.5%; Score 340; DB 15; Length 356;  
Best Local Similarity 100.0%; Pred. No. 3,4e-313;  
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 ILSPMAKGLFKHAKMESGVAIIPLYEAHDYKESDQLQVVAHFCGNNASDSEALACLTCTK 301  
DB 17 ILSPMAKGLFKHAKMESGVAIIPLYEAHDYKESDQLQVVAHFCGNNASDSEALACLTCTK 76  
QY 302 PSKELLTTSQTKSTTRVVDGAFPPNEPLDLSQKAFKAIISIIGVNNHECGFLIPMKEA 361  
DB 77 PSKELLTTSQTKSTTRVVDGAFPPNEPLDLSQKAFKAIISIIGVNNHECGFLIPMKEA 136  
QY 362 PEILSGNKSIALHLIQLNIHLIPQYLHLVANEYHDKSLTEIRDSLLDLGDFVFPVP 421  
DB 137 PEILSGNKSIALHLIQLNIHLIPQYLHLVANEYHDKSLTEIRDSLLDLGDFVFPVP 196  
QY 422 ALITARYHDAAGAPYFYEFRHRPOCFEDTKPAFYKADHAEVRFVFGAFLKGDIVME 481  
DB 197 ALITARYHDAAGAPYFYEFRHRPOCFEDTKPAFYKADHAEVRFVFGAFLKGDIVME 256  
QY 482 GATEBEKLSRKMKYATFARTGNPNNDLSLMPAYNLTEQYQLDLNMSLGORLKEPR 541  
DB 257 GATEBEKLSRKMKYATFARTGNPNNDLSLMPAYNLTEQYQLDLNMSLGORLKEPR 316  
QY 542 VDFMTSTPLILSASDMHSPSLSTPLSLLOPFFPCAP 581  
DB 317 VDFMTSTPLILSASDMHSPSLSTPLSLLOPFFPCAP 356

## RESULT 8

US-10-104-047-2219  
Sequence 2219, Application US/10104047  
Publication No. US20030236392A1  
GENERAL INFORMATION:  
APPLICANT: HELIX RESEARCH INSTITUTE  
TITLE OF INVENTION: No. US20030236392A1 full length cDNA  
FILE REFERENCE: HI-A0105  
CURRENT FILING DATE: 2002-03-25  
PRIOR APPLICATION NUMBER:  
NUMBER OF SEQ ID NOS: 4096  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2219  
LENGTH: 469  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-104-047-2219

Query Match 56.6%; Score 329; DB 15; Length 469;  
Best Local Similarity 99.8%; Pred. No. 1.1e-302;  
Matches 429; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 113 MLKHYYPFGVSEDLTYNITVAPADTGSKLPVLVWFGGAFKTSASIFPGSALAYE 172  
DB 1 MLKHYYPFGVSEDLTYNITVAPADTGSKLPVLVWFGGAFKTSASIFPGSALAYE 60  
QY 173 DVLVVVVYRLGIFGFTTQDHAAGNNAFKDQVVALSWVQNIIEFGDPSVTIFGES 232  
DB 61 DVLVVVVYRLGIFGFTTQDHAAGNNAFKDQVVALSWVQNIIEFGDPSVTIFGES 120  
QY 233 AGAIVSSLLISPMKGLFKHAKMESGVAIIPLYEAHDYKESDQLQVVAHFCGNNASDSE 292  
DB 121 AGAIVSSLLISPMKGLFKHAKMESGVAIIPLYEAHDYKESDQLQVVAHFCGNNASDSE 180

QY 293 ALLRLCTKPSKELLTTSQTKSTTRVVDGAFPPNEPLDLSQKAFKAIISIIGVNNHEC 352  
DB 181 ALLRLCTKPSKELLTTSQTKSTTRVVDGAFPPNEPLDLSQKAFKAIISIIGVNNHEC 240  
QY 353 GFLIPMKEAPBILSGNKSIALHLIQLNIHLIPQYLHLVANEYHDKSLTEIRDSLLDL 412  
DB 241 GFLIPMKEAPBILSGNKSIALHLIQLNIHLIPQYLHLVANEYHDKSLTEIRDSLLDL 300  
QY 413 LGDVFVFPALITARYHDAAGAPYFYEFRHRPOCFEDTKPAFYKADHAEVRFVFGAF 472  
DB 301 LGDVFVFPALITARYHDAAGAPYFYEFRHRPOCFEDTKPAFYKADHAEVRFVFGAF 360  
QY 473 LKGDIVMEGATEBEKLSRKMKYATFARTGNPNNDLSLMPAYNLTEQYQLDLNMS 532  
DB 361 LKGDIVMEGATEBEKLSRKMKYATFARTGNPNNDLSLMPAYNLTEQYQLDLNMS 420  
QY 533 LGORLKEPRV 542  
DB 421 LGORLKEPRV 430

## RESULT 9

US-10-114-270-196  
Sequence 196, Application US/10114270  
Publication No. US20040030110A1  
GENERAL INFORMATION:  
APPLICANT: Guo, Xiaojia  
APPLICANT: Kekuda, Rameesh  
APPLICANT: Miller, Charles E.  
APPLICANT: Malysankar, Uriel M.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Paturajan, Meera  
APPLICANT: Liu, Ziaohong  
APPLICANT: Gusev, Vladimr Y.  
APPLICANT: Li, Li  
APPLICANT: Vernec, Corine  
APPLICANT: Zernusen, Bryan D.  
APPLICANT: Gorman, Linda  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Pena, Carol E.A.  
APPLICANT: Smithson, Glenda  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Shinkens, Richard A.  
APPLICANT: Gangolli, Esna A.  
APPLICANT: Taupier Jr., Raymond J.  
APPLICANT: Caeman, Stacie J.  
APPLICANT: Ji, Weizhen  
APPLICANT: Anderson, David W.  
APPLICANT: Liette, Mario W.  
APPLICANT: Raestelli, Luca  
APPLICANT: Edinger, Shlomil R.  
APPLICANT: Stone, David J.  
APPLICANT: MacDougall, John R.  
APPLICANT: Rothenberg, Mark E.  
TITLE OF INVENTION: No. US20040030110A1 Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-322C  
CURRENT APPLICATION NUMBER: US/10/114,270  
CURRENT FILING DATE: 2002-11-27  
PRIOR APPLICATION NUMBER: 60/281,086  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/281,136  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/281,863  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/281,906  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/282,020  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: 60/282,930  
PRIOR FILING DATE: 2001-04-10  
PRIOR APPLICATION NUMBER: 60/282,934

;; PRIOR FILING DATE: 2001-04-10  
;; PRIOR APPLICATION NUMBER: 60/283,512  
;; PRIOR FILING DATE: 2001-04-12  
;; PRIOR APPLICATION NUMBER: 60/283,710  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/284,234  
;; PRIOR FILING DATE: 2001-04-17  
;; Remaining Prior Application data removed - See file Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 470  
;; SEQ ID NO 196  
;; LENGTH: 581  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-114-270-196

Query Match 56.5%; Score 328; DB 15; Length 581;  
Best Local Similarity 100.0%; Pred. No. 1.2e-301;  
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 31 GPSAEGPQRTNRLGWIQKQVTVLGSPPVNVFLGVPFAAPPLGSLRFTNPQASPMDNL 90  
DB 27 GPSAEGPQRTNRLGWIQKQVTVLGSPPVNVFLGVPFAAPPLGSLRFTNPQASPMDNL 86  
QY 91 REATSYPNCLQNSEWLLDDQHLKVHYPKFGVSEDCLYINITYAPAHADTGSKLPVLWF 150  
DB 87 REATSYPNCLQNSEWLLDDQHLKVHYPKFGVSEDCLYINITYAPAHADTGSKLPVLWF 146  
QY 151 PGGAFTGASIFDGSALAAVEDVLVVVQYRLGIFGFTTWDQAPGNMAFKQVVALS 210  
DB 147 PGGAFTGASIFDGSALAAVEDVLVVVQYRLGIFGFTTWDQAPGNMAFKQVVALS 206  
QY 211 WYQKNIFFGDPSSVTIFGSAAGISVSLILSPMAKGLFHKAIMESGVAIIPLYLAHD 270  
DB 207 WYQKNIFFGDPSSVTIFGSAAGISVSLILSPMAKGLFHKAIMESGVAIIPLYLAHD 266  
QY 271 YKSEDLQVVAHFCGNMNSDEALLRCLRTKPSKELLTSOKTSPFRVVDGAFFPNEPL 330  
DB 267 YKSEDLQVVAHFCGNMNSDEALLRCLRTKPSKELLTSOKTSPFRVVDGAFFPNEPL 326  
QY 331 DLSQAKFAKAIPIIIGVNNHECGFLPM 358  
DB 327 DLSQAKFAKAIPIIIGVNNHECGFLPM 354

RESULT 10  
US-10-451-168-92  
;; Sequence 92, Application US/10451168  
;; Publication No. US20040091969A1  
;; GENERAL INFORMATION:  
;; APPLICANT: SMITHKLINE BEECHAM CORPORATION  
;; APPLICANT: SMITHKLINE BEECHAM P.L.C.  
;; TITLE OF INVENTION: NOVEL COMPOUNDS  
;; FILE REFERENCE: GPS0039  
;; CURRENT APPLICATION NUMBER: US/10/451,168  
;; PRIOR FILING DATE: 2003-11-12  
;; PRIOR APPLICATION NUMBER: PCT/US01/49232  
;; PRIOR FILING DATE: 2000-12-17  
;; PRIOR APPLICATION NUMBER: 60/256,710  
;; PRIOR FILING DATE: 2000-12-19  
;; PRIOR APPLICATION NUMBER: 60/257,048  
;; PRIOR FILING DATE: 2000-12-20  
;; PRIOR APPLICATION NUMBER: 60/260,482  
;; PRIOR FILING DATE: 2001-01-09  
;; PRIOR APPLICATION NUMBER: 60/264,922  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: 60/266,797  
;; PRIOR FILING DATE: 2001-02-06  
;; PRIOR APPLICATION NUMBER: 60/276,988  
;; PRIOR FILING DATE: 2001-03-19  
;; PRIOR APPLICATION NUMBER: 60/281,535  
;; PRIOR FILING DATE: 2001-04-04  
;; PRIOR APPLICATION NUMBER: 60/289,622

;; PRIOR FILING DATE: 2002-06-28  
;; NUMBER OF SEQ ID NOS: 110  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 92  
;; LENGTH: 581  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-451-168-92

Query Match 56.5%; Score 328; DB 15; Length 581;  
Best Local Similarity 100.0%; Pred. No. 1.2e-301;  
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 31 GPSAEGPQRTNRLGWIQKQVTVLGSPPVNVFLGVPFAAPPLGSLRFTNPQASPMDNL 90  
DB 25 GPSAEGPQRTNRLGWIQKQVTVLGSPPVNVFLGVPFAAPPLGSLRFTNPQASPMDNL 84  
QY 91 REATSYPNCLQNSEWLLDDQHLKVHYPKFGVSEDCLYINITYAPAHADTGSKLPVLWF 150  
DB 85 REATSYPNCLQNSEWLLDDQHLKVHYPKFGVSEDCLYINITYAPAHADTGSKLPVLWF 144  
QY 151 PGGAFTGASIFDGSALAAVEDVLVVVQYRLGIFGFTTWDQAPGNMAFKQVVALS 210  
DB 145 PGGAFTGASIFDGSALAAVEDVLVVVQYRLGIFGFTTWDQAPGNMAFKQVVALS 204  
QY 211 WYQKNIFFGDPSSVTIFGSAAGISVSLILSPMAKGLFHKAIMESGVAIIPLYLAHD 270  
DB 205 WYQKNIFFGDPSSVTIFGSAAGISVSLILSPMAKGLFHKAIMESGVAIIPLYLAHD 264  
QY 271 YKSEDLQVVAHFCGNMNSDEALLRCLRTKPSKELLTSOKTSPFRVVDGAFFPNEPL 330  
DB 265 YKSEDLQVVAHFCGNMNSDEALLRCLRTKPSKELLTSOKTSPFRVVDGAFFPNEPL 324  
QY 331 DLSQAKFAKAIPIIIGVNNHECGFLPM 358  
DB 325 DLSQAKFAKAIPIIIGVNNHECGFLPM 352

RESULT 11  
US-10-381-898-2  
;; Sequence 2, Application US/10381898  
;; Publication No. US2004008687A1  
;; GENERAL INFORMATION:  
;; APPLICANT: AZIMZAI, Yalda; BAUGHN, Mariah R.;  
;; APPLICANT: BOROWSKY, Mark L.; DING, Li;  
;; APPLICANT: DUGGAN, Brendan; ELLIOTT, Vicki S.;  
;; APPLICANT: GANDHI, Ameena R.; GRIFFIN, Jennifer A.;  
;; APPLICANT: HAPALIA, April J.A.; ISON, Craig H.;  
;; APPLICANT: KHAN, Farrah A.; LAL, Preeti G.;  
;; APPLICANT: LEE, Ernestine A.; LU, Dyung Alina M.;  
;; APPLICANT: RAMKUMAR, Jayalaxmi; RING, Huijun Z.;  
;; APPLICANT: SANJANWALA, Madhusudan M.;  
;; APPLICANT: TANG, Y. Tom; TRIBUNEY, Catherine M.;  
;; APPLICANT: CHAWLA, Narinder K.; WALSH, Roderick T.;  
;; APPLICANT: WARREN, Bridget; XU, Yuming;  
;; APPLICANT: YANG, Juming; YAO, Monique; YUE, Henry  
;; TITLE OF INVENTION: DRUG METABOLIZING ENZYMES  
;; FILE REFERENCE: PI-0233 USN  
;; CURRENT APPLICATION NUMBER: US/10/381,898  
;; PRIOR FILING DATE: 2003-10-17  
;; PRIOR APPLICATION NUMBER: PCT/US01/30662  
;; PRIOR FILING DATE: 2001-09-28  
;; PRIOR APPLICATION NUMBER: US 60/236,947  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: US 60/238,864  
;; PRIOR FILING DATE: 2000-10-06  
;; PRIOR APPLICATION NUMBER: US 60/242,323  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: US 60/247,581  
;; PRIOR FILING DATE: 2000-11-09  
;; PRIOR APPLICATION NUMBER: US 60/249,519  
;; PRIOR FILING DATE: 2000-11-16



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;; PRIOR APPLICATION NUMBER: US 60/252,834
;; PRIOR FILING DATE: 2000-11-22
;; PRIOR APPLICATION NUMBER: US 60/250,567
;; PRIOR FILING DATE: 2000-11-30
;; NUMBER OF SEQ ID NOS: 36
;; SOFTWARE: PERL Program
;; SEQ ID NO 2
;; LENGTH: 618
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; OTHER INFORMATION: Incyte ID No: 7473645CD1
US-10-381-898-2

Query Match      56.5%; Score 328; DB 15; Length 618;
Best Local Similarity 100.0%; Pred. No. 1.3e-301;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 GPSAEGPQNRTRLGMIOGKQVTVLGSPPVNVNVLGVPAPPLGSLRFTNPQASPMDNL 90
Db 92 GPSAAGPQNRTRLGMIOGKQVTVLGSPPVNVNVLGVPAPPLGSLRFTNPQASPMDNL 151
Qy 91 REATSYPMULCLQNSWMLLDQMLKVHYPKRGVSBDCLYLNITYAPAHADTGSKLPLYWF 150
Db 152 REATSYPMULCLQNSWMLLDQMLKVHYPKRGVSBDCLYLNITYAPAHADTGSKLPLYWF 211
Qy 151 PGGAFTKTSASIFDGSALAAVEDVTVVVOYRLGIFGFFTTMDQHPGNMAFKDOVAALS 210
Db 212 PGGAFTKTSASIFDGSALAAVEDVTVVVOYRLGIFGFFTTMDQHPGNMAFKDOVAALS 271
Qy 211 WVKQNIFFGGDPSSVTIFGESAGASVSSLLISPMAGLFFKAIMESGVALIPLYEAHD 270
Db 212 WVKQNIFFGGDPSSVTIFGESAGASVSSLLISPMAGLFFKAIMESGVALIPLYEAHD 331
Qy 271 YEKSEDLQVVAHFCGNNAASDSEALIRCLRTKPSKELLTISOXTKSFTRVVDGAFPPNEPL 330
Db 332 YEKSEDLQVVAHFCGNNAASDSEALIRCLRTKPSKELLTISOXTKSFTRVVDGAFPPNEPL 391
Qy 331 DLSQAKAFKAPSIIGVNNHCEGFLPM 358
Db 392 DLSQAKAFKAPSIIGVNNHCEGFLPM 419

RESULT 12
US-09-864-761-36376
;; Sequence 36376, Application US/09864761
;; Patent No. US20020048763A1
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharon G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wenheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: Aecmiga-X-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
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;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 36376
;; LENGTH: 49
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC007335.2
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
;; OTHER INFORMATION: EXPRESSED IN HELI00, SIGNAL = 2.5
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
;; OTHER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 2.2
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.1
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.4
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
;; OTHER INFORMATION: EST HUMAN HIT: AV650422.1, EVALUE 2.00e-09
;; OTHER INFORMATION: SWISSPROT HIT: Q04791, EVALUE 2.00e-11
US-09-864-761-36376

Query Match      8.4%; Score 49; DB 9; Length 49;
Best Local Similarity 100.0%; Pred. No. 3.5e-38;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 432 AGAPYFYEFRRHPQCFEDTTPAFVKADHADEVRFVGGATLKGDIVWF 480
Db 1 AGAPYFYEFRRHPQCFEDTTPAFVKADHADEVRFVGGATLKGDIVWF 49

RESULT 13
US-10-233-933A-2
;; Sequence 2, Application US/10233933A
;; Publication No. US20040214171A1
;; GENERAL INFORMATION:
;; APPLICANT: Yamashita, Tetsuro
;; APPLICANT: Miyazaki, Masao
;; TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER
;; FILE REFERENCE: SHIG PPO2US006
;; CURRENT APPLICATION NUMBER: US/10/233,933A
;; CURRENT FILING DATE: 2002-09-03
;; PRIOR APPLICATION NUMBER: JP2002-051908
;; PRIOR FILING DATE: 2002-04-03
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 542
;; TYPE: PRT
;; ORGANISM: Felis catus
US-10-233-933A-2
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Query Match 5.3%; Score 31; DB 16; Length 542;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-20;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 465 RFVFGAFLKGDIVMEGATEEEKLSRKM 495  
 DB 456 RFVFGAFLKGDIVMEGATEEEKLSRKM 486

## RESULT 14

US-10-233-933A-4  
 ; Sequence 4, Application US/10233933A  
 ; Publication No. US20040214171A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yamashita, Tetsuro  
 ; APPLICANT: Miyazaki, Masao  
 ; TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER  
 ; FILE REFERENCE: SHIG FP02US006  
 ; CURRENT APPLICATION NUMBER: US/10/233,933A  
 ; PRIOR FILING DATE: 2002-09-03  
 ; PRIOR APPLICATION NUMBER: JP2002-057908  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 542  
 ; TYPE: PR1  
 ; ORGANISM: Felis catus  
 US-10-233-933A-4

Query Match 5.3%; Score 31; DB 16; Length 542;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-20;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 465 RFVFGAFLKGDIVMEGATEEEKLSRKM 495  
 DB 456 RFVFGAFLKGDIVMEGATEEEKLSRKM 486

Search completed: June 16, 2005, 21:18:08  
 Job time : 160 secs